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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 20, 2004, 13:07:24 ; Search time 17 Seconds (without alignments) 1175.668 Million cell updates/sec

US-09-680-121C-2
2201
1 MAPITTSREEEPDEIPTVVGI......KEICDYPRRQIAKWHVLCDG 425 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES Resi

		iption	O9h2b2 homo ganien	rattr	P40749 mus musculu	mus m	Q9bt88 homo sapien	rattn		P21521 drosophila	homo sar			P29101 rattus norv				_	mu8	bog	homod	O9r0n5 mus musculu	rat	P24505 discopyge o		P24506 discopyge o		000445 homo sapien			-	pos	omor c	mus	9 ratt
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		Match Length		425	425	430	431	430	403	4/4	402	426	422	422	537	441	498	523	421	422	422	386	421	427	424	439	386	386	288	590	587	704	694	681	8
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SYTB_MOUSE YPT7_CABEL PCLO_CHICK PCLO_HUMAN PCLO_HUMAN PCLO_MOUSE PCLO_MOUSE RCG_RABIT KPCG_RABIT KPCG_RABIT KPCG_RABIT KPCG_HUMAN KPCG_HUMAN KRCG_MOUSE RSGS_HUMAN RSGS_HUMAN
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0 1 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2 1 2
361.5 332 192.5 184.5 181.5 180.1 179.5 179.5 177.5 177.5

## ALIGNMENTS

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CYTOPLASMIC (POTENTIAL)
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PROSITE; PS50004; C2 DOMAIN 2; 2.
Transmembrane; Repeat; Synapse.
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PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synaptotagmin IV (SytIV).
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
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37
425
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 600103; -.

R GO; GO:0016021; C:integral to membrane; ISS.

BG; GO:00161158; P:regulation of calcium ion dependent exocytosis; ISS.

BR GO; GO:0016181; P:synaptic vesicle transport; ISS.

BR InterPro; IPR002049; C2.

BR InterPro; IPR001549; LRI.

BR PROSTE; PR001565; Synaptotagmin.

BR PROSTE; PR00199; SYNAPTOTAGMN.

BR PROSTE; PS00499; C2 DOMAIN 1; 2.

BR PROSTE; PS0004; C2 DOMAIN 1; 2.

BR PROSTE; PS0004; C2 DOMAIN 2; 2.

KW Transmembrane; Repeat; Synapse.

FT DOMAIN 17 37 POTENTIAL.

FT TRANSMEM 17 37 CYMODIASMIC (POTENTIAL).
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C2 domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis.
SUBCELLUIAR LOCATION: Integral membrane protein. Synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٥:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHOLIPID BINDING (PROBABLE)
C2 DOMAIN 1.
C2 DOMAIN 2.
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                                                                                                                                                         IN AMYGDALA AND THALAMUS.
--- SIMILARITY: Contains 2 C2 domains.
--- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2201; DB 1;
Pred. No. 6.4e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF299075; AAG37229.1; -.
EMBL; AB037763; BAA92580.1; ALT_INIT.
EMBL; BC036538; AAH36538.1; -.
HSSP; P21707; 1BYN.
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MIM; 600103; -.
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147
155
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425 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U14398; AAA68519.1; --
EMBL; L38247; AAA67327.1; --
EMBL; L38247; AAA67327.1; --
EMBL; L38247; AAA67327.1; --
EMBL; L3825; L3935.
HSSP; P21707; L1BV
GO; GO:0016021; C:integral to membrane; ISS.
GO; GO:0016181; P:Frgulation of calcium ion dependent exocytosis; ISS.
GO; GO:0016181; P:Frgulation of calcium ion dependent exocytosis; ISS.
InterPro; IPR000008; C2.
InterPro; IPR00169; C2.
InterPro; IPR001565; Synaptotagmin.
Flam; PF00168; C2; 2.
Fram; F000168; C2; 2.
Fram; F000168; C2; 2.
                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=95085772; PubMed=7993622;
Ullrich B., Li C., Zhang J.Z., McMahon H., Anderson R.G., Geppert Suedhof T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional properties of multiple synaptotagmins in brain."; Neuron 13:1281-1291(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
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                                               (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
425 AA
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                                                                                                                              MGD; MGI:101759; Syt4.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:001158; P:regulation of calcium ion dependent exocytosis; TAS.

GO; GO:0016181; P:synaptic vesicle transport; TAS.

InterPro; IPR00008; C2.

InterPro; IPR002149; IRI.

InterPro; IPR001565; Synaptotagmin.

Ffam; PF00168; C2; 2......
                                                                                                                                                                                                                                                                                                                                                         PHOSPHOLIPID BINDING (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                            D1900D475C163821 CRC64;
                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                  VESICULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ....
                                                                                                                                                                                                                                                                                                                                                                                                                     90.3%; Score 1988; DB 1;
89.4%; Pred. No. 3.3e-130;
11ve 21; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                   C2 DOMAIN 1.
                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                      PEAM; PF00168; C2; 2.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGNN.
SMART; SM00239; C2; 2.
PROSITE; PS00499; C2 DOMAIN 1; 2.
PROSITE; PS50004; C2 DOMAIN 2; 2.
Transmembrane; Repeat; Synapse.
                                                                                                                                                                                                                                                                                                                                                                                            47630 MW;
                                                                                                          EMBL; U10355; AAA20971.1; -.
HSSP; P21707; 1BYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                  16
37
425
297
258
392
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38
147
155
289
425 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             380;
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TRANSMEM
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SEQUENCE
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                                                                                                                                                                                 121 ATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGL 180
                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                    PAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHF 240
                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                      TILSFDRFSRDDIIGEVLIPLSGIELSEGKMLANREIIKRNVRKSSGRGELLISLCYQST 300
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                                                                                                                                       1 MAPITISRVEFDEIPTVVGIFSAFGLVFTVSLFAWICCORRSAKSNKTPPYKFVHVLKGV
                                                                                                                                                                                                                                           121 VTPKLFPETEKBAVSPESLKSSTSLTSEEKQEKLGTLFLSLEYNFEKKAFVVNIKEAQGL
                                                                                                                                                                                                                                                                                     DIPCEGLEDISVEFLVLDSERGSRNEVIGOLVLGAAAEGTGGEHWKEICDYPRRQIAKWH
                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SPECIFICITY: EXPRESSED IN MANY REGIONS OF THE NERVOUS SYSTEM BUT IS UNDETECTABLE IN EXTRA NEURAL TISSUES. SIMILARITY: Contains 2 C2 domains. SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilbush B.S., Morgan J.I.,
"A third synaptotagmin gene, Syt3, in the mouse.",
Proc. Natl. Acad. Sci. U.S.A. 91:8195-8199(1994).
-!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of
secretory vesicles through Ca(2+) and phospholipid binding t
C2 domain or may serve as Ca(2+) sensors in the process of
vesicular trafficking and exocytosis.
-!- SUBCELBULAR LOCATION: Integral membrane protein. Synaptic
                                                                                            ;
0
                                                                   425;
     PHOSPHOLIPID BINDING (PROBABLE)
                                                               91.1%; Score 2006; DB 1; Length 4
89.9%; Pred. No. 1.9e-131;
ive 21; Mismatches 22; Indels
             C2 DOMAIN 1.
C2 DOMAIN 2.
6AC88E00878936BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
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01-FEB-1995 (Rel. 31, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425
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STRAIN-BALB/c; TISSUE-Brain;
MEDLINE-94336712; PubMed-8058779;
                                       47685 MW;
                                                                                        Matches 382; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, La Synaptotagmin IV (SytIV)
   297
258
392
 147
155
289
425 AA;
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLCDG 425
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MLCDG 425
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28-FEB-2003
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P40749;
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SEQUENCE 1
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                                       SEQUENCE
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                                                               Query Match
                                                                           Best Local
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 DOMAIN
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0 120 240 300 DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLEN 120 ATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGL 180 121 VTPKLFTETEKEANSPESLKSSTSLTSEEKQEKLGTLFLSLEYNFEKKAFVVNIKEAQGL 180 240 300 360 360 420 9 9 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLFAWICCQRKSSKSNKTPPXKFVHVLKGV 1 MAPITISRVEFDEIPTVVGIFSAFGLVFTVSLFAMICCQRRSAKSNKTPPYKFVHVLKGV 61 DIYPENLSSQKKREGGDDKSEVKGKTALPNLSLHLDLEKRDLNGNFPKANPKAGSSSDLEN PAMDEQSMISDPYIKMIILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQBLALHF TILSFDRESRDDIIGEVLIPLSGIELSEGKMLMMREIIKRNVRKSSGRGELLISLCYQST TNTL TVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRI SKKKTHVKKCTPNAVFNELFVF 301 INTLITVIVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVF DIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKWH Gaps .; Length 425; Ą 430 PRT; SYTB MOUSE Q9R0N3; SYTB MOUSE ID SYTB MC AC Q9R0N3; =

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                      SYTB HUMAN
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SYTE HUMAN
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 LHLDLEKRDLNGNF---PKTNLKPGSPSDLENATPKLFLEGEKESVSPESLKSSTSLTSEE 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 KQEKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTR 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAEITKIRPSFDVSPVAAGLIGASVLVVCVSVTVFVWTCCHQQAEKKHKTPPVKFIHMLK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAPITISREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCORKSSKSNKTPPYKFVHVLK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FGADDKNEVKNKPAVPKNS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ICR; TISSUE-Cerebellum;
MEDLINE=2002669; PubMed=10531343;
Fukuda M., Kanno E., Mikoshiba K.;
"Conserved N-terminal cysteine motif is essential for homo- and heterodimer formation of synaptotagmins III, V, VI, and X.";
J. Biol. Chem. 274.31421.31427(1999).
-!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of secretory vesicles through Ca(2+) and phospholipid binding to C3 domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis (By similarity).
-!- SUBURIT: Homodimer. Can also form heterodimer (By similarity).
-!- SUBCELIULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.0%; Score 1167.5; DB 1; Length 430; 51.0%; Pred. No. 1.7e-73; ive 70; Mismatches 93; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
C2 DOMAIN 1.
C2 DOMAIN 2.
25E7CDFC4B4BE036 CRC64;
                                                                                                                                                                                                                                                                                                       VESICLES (By similarity).
SIMILARITY: Contains 2 C2 domains.
SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1859547; Syt11.
GO; GO:0005887; C:integral to plasma membrane; IDA.
InterPro; IPR000008; C2.
InterPro; IPR001149; IRI.
InterPro; IPR001165; Synaptotagmin.
PF00168; C2: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VESICULAR (POTENTIAL)
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-PEB-2003 (Rel. 41, Last annotation update)
Synaptotagmin XI (SytXI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVDIYPENLNSKKK-----
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PROSITE; PS50004; C2_DOMAIN_2; 2.
Transmembrane; Repeat; Synapse.
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB026808; BAA85780.1; -. HSSP; P21707; 1RSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
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Matches 233; Conservative
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396
                                                                  Mus musculus (Mouse)
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37
173
2
303
430 AA;
                                                                                                                                SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=10090;
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SEQUENCE
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153 EDVMLGSLIFSVDYNFPKKALVVTIQEAHGLPVMDDQTQGSDPYIKMTILPDKRHRVKTR 212
                                                                                                                                                                                                                                                           270 KMLMNREIIKRNVRKSSGRGELLISLCYQSTINTLIVVVULKARHLPKSDVSGLS-DPYVK 328
                                                                                                                                                                                                                                                                                                                 RECTISSUE=Brain, and Lymph;

RX TISSUE=Brain, and Lymph;

RX Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hahteh F.,

RA Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Matusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Browstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Browstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Wullahy S.J.,

RA Bromstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Wullahy S.J.,

RA Bromstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gabus R.A.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gabusa R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Willalon D.K., Murmy D.M., Scheuren E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Ritcrifield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Generation and initial analysis of more than 15,000 full-length

Ruhan and mouse Chry sequences.",

Recretcry vesicles trafficking and exocytosis of secretory vesicles in Involved in Ca(2+) and phospholipid binding to the

CC domain or may serve as Ca(2+) and phospholipid binding to the

CC C domain or may serve as Ca(2+) sensors in the process of

Vesicular trafficking and exocytosis (By similarity).

CL SUBUSELLULAR LOCATION: INTEGRAL MEMBRANE PROTÉIN. SYNAPTIC

VESICLES (By similarity).

CL SIMILARITY: Contains 2 C2 domains.
                                                                                                                                  213 VLRKTLDPVFDETFTFYGIPYSQLQDLVLHFLVLSFDRFSRDDVIGEVWVPLAGVDPSTG
                                                                                     210 VLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                      VNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             389 GOLVLGAAAEGT-GGEHWKEICDYPRROIAKWHVLCD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [6-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last Bequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-2003 (Rel. 42, La Synaptotagmin XI (SytXI)
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VESICLES
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                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                             GVDIYPENLNSKKKF-----GADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPG
                                                                                                                                                                                                                                                                                                                                                                                  FVVNIKEARGLPAMDEQSMTSDPYIKWTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRG
                                                                                                                                                                                                                                                                                                                                 MAPITTSREEPDEIPTVVGIFSAFGLVFTVS--LFAWICCQRKSSKSNKTPPYKFVHVLK
                                                                                                                                                                                                                                                                                                                                                                                                          SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKA
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                               Length 431;
                                                                                                                                                                                                                                                                                            52.8%; Score 1162; DB 1; Length 4
52.4%; Pred. No. 4e-73;
tive 77; Mismatches 111; Indels
                                                                                                                                                                                                                                                                          A7F76AD745C0FF7D CRC64;
SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY
                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                             VESICULAR (POTENTIAL)
                                                                                                                                      InterPro; IPR000008; C2.
InterPro; IPR001008; C2.
InterPro; IPR001565; Synaptotagmin.
Pfam; PF00168; C2; 2.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SW00399; SYNAPTOTAGMN.
PROSITE; PS00499; C2 DOMAIN 1; FALSE_NEG.
PROSITE; PS50004; C2_DOMAIN 2; 2.
                                                                                                                                                                                                                                                         C2 DOMAIN 1
C2 DOMAIN 2
                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                 Transmembrane; Repeat; Synapse.
DOMAIN 1 15 VE
TRANSMEM 16 36 PO
                                                                                         EMBL; AK074931; BAC11300.1; -.
EMBL; BC004291; AAH04291.1; -.
EMBL; BC013690; AAH13690.1; -.
                                                                                                                                                                                                                                                                          48306 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408 ICDYPRRQIAKWHVLCD 424
                                                                                                                               Genew; HGNC:19239; SYT11.
                                                                                                                                                                                                                                                                                                             Matches 229; Conservative
                                                                                                                     HSSP; P21707; 1RSY.
                                                                                                                                                                                                                                                                         431 AA;
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                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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61 GISIYPETLSNKKEIIKVRRDKDGSHRESGRGNLLVNAÆSGILLSHDRDPRGPSPASCIDQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 GVDIYPENINSKKKFGADDKNEVKNKPAVPKNSLHLDLEK-----RDLNGNFP----- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166
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                                                                                                                                                                                                                                                                                                                 TISSUE=Brain,
MEDLINE=97306341; PubMed=9162066;
WEDLINE=97306341; PubMed=9162066;
von Poser C., Ichtchenko K., Shao X., Rizo J., Suedhof T.C.;
"The evolutionary pressure to inactivate. A subclass of synaptotagmins with an amino acid substitution that abolishes Ca2+ binding.";
With an amino acid substitution that abolishes Ca2+ binding.";
J. Biol. Chem. 272:14314-14319(1997).

-!- FUNCTION: May be involved in Ca(2+) dependent exocytosis of secretory vesicles through Ca(2+) and phospholipid binding to the secretory vesicles through Ca(2+) sensors in the process of ca domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: Highly expressed in brain and at lower levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAEITNIRPSFDVSPVAAGLIGASVLVVCVSVTVFVWTCCHQQAEKKHKTPPYKFIHMLK
                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAPITISREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCQRKSSKSNKTPPYKFVHVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 ---KTNLKPGSPSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SSPEEDVMLGSLTFSVDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homodimer. Can also form heterodimer (By similarity)
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
VRSTOTISS (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
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51.5%; Pred. No. 9.6e-73;
.ive 78; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C2 DOMAIN 1.
C2 DOMAIN 2.
C1FA13CB9177C825 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in other tissues.
-1- SIMILARITY: Contains 2 C2 domains.
-i- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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16-OCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Synaptotagmin XI (SytXI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00008; C2.
InterPro; IPR00149; LRI.
InterPro; IPR001565; Synaptotagmin.
Pfam; PR00168; C2; 2.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM0239; C2; 2.
PROSITE; PS00499; C2_DOMAIN_1; FALSE_NEG.
PROSITE; PS50004; C2_DOMAIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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37 430 CYT
158 261 CZ
292 396 C2
430 AA, 48268 MW; (
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DOWALN
1 15 VE
TRANSMEM 16 36 PO
DOWALN 37 430 CY
DOMAIN 158 261 C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF000423; AAB58344.1; -.
                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity
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                                                                                                                                    (Rat)
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P21707; 1RSY
                                                                                                                                                                                                                           NCBI TaxID=10116;
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226

430 AA.

PRT;

SYTB RAT STANDARD; 008835; 16-OCT-2001 (Rel. 40, Created)

SYTE RAT

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SY65
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TEYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVR 283
                                   284 KSSGRGELLISLCYQSTINTLIVVVIKARHLPKSDVSGLS-DPYVKVNLYHAKKRISKKK 342
                                                                                                                                                                          406
                                                                                                                                                                                                                                                                          THVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGT-G 401
                                                                                                                                                                                                                                                                                                                 to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQUENCE FROM N.A.

C STRAIN=ICR; INSUB—Cerebellum;

MEDLINE=2002669; PubMed=1053143;

MEDLINE=2002669; PubMed=1053143;

Fukuda M., Kanno B., Mikoshiba K.;

"Conserved N-terminal cysteine motif is essential for homo- and

"Conserved N-terminal cysteine motif is essential for homo- and

"Conserved N-terminal cysteine motif is essential for homo- and

"Conserved N-terminal cysteine motif is essential for homo- and

"Conserved N-terminal cysteine motif is essential for homo- and

"Conserved N-terminal Cysteine (37,1)

"I Biol. Chem. 274:31427-1499;

"I Biol. Chem. 274:31427-1999;

"I Biol. Chem. 274:31427-1999;

"C domain or may serve as Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) and phospholipid binding to the Vesicular trafficking and exocytosis (By similarity).

"USSICILES (By similarity).

"I SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
C2 DOMAIN 1.
C2 DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VESICULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Synaptotagmin VII (SytVII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403 AA.
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InterPro; IPR001008; C2.

InterPro; IPR001149; LRI.

InterPro; IPR001165; Synaptotagmin.

Pfam; PF01168; C2; 2.

PRINTS; PR00399; C2 DOMAIN.

PROSITE; PS00499; C2 DOMAIN 1; 2.

PROSITE; PS50049; C2 DOMAIN 1; 2.

TRANSMEM 17 37 PSCIULAL 16 DOMAIN 18 37 POTENTIAL DOMAIN 137 C2 DOMAIN 137 POTENTIAL DOMAIN 137 C2 DOMAIN 137 C3 DOMAIN 137 C2 DOMAIN C2 DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                     407 AEHWREVCESPRKPVAKWHSLSE 429
                                                                                                                                                                                                                                                                                                                                                                                                                     GEHWKEICDYPRRQIAKWHVLCD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB026804; BAA85776.1;
HSSP; P21707; IRSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYT7 MOUSE
                                                                                                                                                                                                                                                                              343
                                                                                                                                                                                                                                                                                                                                                                                                                     402
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                  78 ----KNEVK-----NKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENATPK 124
                                                                                                                                                                                                                                                                                                                                                                               125 LFLEGEKESVSPESLKSSTSLTSEE-----KQEKLGTLFFSLEYNFERKAFVVNIKEARG 179
                                                                                                                                                                                                                                                                                                                                                                                                                      110 -----SLTSEMLMLSPGSEEDEAHEGCSRENLGRIQFSVGYNFQESTLIVKVMKAQE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                       -----NSLETVGTPDSG
                                                                                                                                                          27 VFTVSL----FAWIC--CQRKSSKSNKTPPYKFVHVLKGVDIYPENLNSKKKFGADD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 FTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQS
                                                                                                                                                                                                                                                                                                                          63 RGRGEKKAIKLPAGGKAVNTAPVÞGQTPHDESDRR-----TETR-SSVSDLVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 LPAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 TINILIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 FDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila and humans.",
J. Biol. Chem. 266:615-622(1991).
-!- FUNCTION: MAY HAVE A REGILATORY ROLE IN THE MEMBRANE INTERACTIONS
DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEGUENCE FROM N.A.
MEDLINE=91093190; PubMed=1840599;
Perin M.S., Johnston P.A., Oezcelik T., Jahn R., Francke U.,
Suedhof T.C.;
"Structural and functional conservation of synaptotagmin (p65) in
                                                                                                                71;
                                                     28.5%; Score 627.5; DB 1; Length 403; 36.2%; Pred, No. 3.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                Indels
  45472 MW; 4E63C5779C2ED43E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
-!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                          71; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä.
                                                                                                                                                                                                               23 IITVSLSVTIVLCGLCHWCORKLGKRYK-
                                                                                                       Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synaptotagmin (p65).
403 AA;
                                               Query Match
Best Local Similarity
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SEQUENCE
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P21521;
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MIM; 604146; -.
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  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 FVHVLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLBKRDLNGNFPKTNLKP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 GSPSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 NIKEARGLPAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 IQELALHFIILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGR---G 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 PNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEIC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PITISREEFDEIPTVV-----GIFSAFGLVFTVSLFAWICCORKSSKSNKTPPYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVIKKIEHVGEVVTEVIAERTGLPTWGVVAIIILVPLVVFGIIFFCVRRFLKKRRTK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AMNKTLVFAIFDFDRFSKHDQIGEVKVPLCTIDLAQ-TIEEWRDLV--SVEGRGGGEKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 ELLISLCYQSTINTLIVVVILKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                          R GO; GO:0030285; C:integral to synaptic vesicle membrane; NAS.
R GO; GO:0030285; C:integral to synaptic vesicle membrane; NAS.
R GO; GO:000345; P:larval locomotory behavior; IMP.
R GO; GO:0007317; P:regulation of pole plasm oskar mRNA localiz. ..;
R GO; GO:0016083; P:ragulation of pole plasm oskar mRNA localiz. ..;
R GO; GO:0016083; P:ragulation of pole plasm oskar mRNA localiz. ..;
R GO; GO:0016083; P:ragulation of pole plasm oskar mRNA localiz. ..;
R InterPro; IPR001089; C2.
InterPro; IPR001565; Synaptotagmin.
R PRINTS; PR001369; SYNAPTOTAGMN.
R PRINTS; PR00399; SYNAPTOTAGMN.
R PROSITE; PS00499; C2; ZDOMAIN. 1; Z.
RPGSITE; RS00499; C2; DOMAIN. 1; Z.
RPGSITE; PS050049; C2 DOMAIN. 2; Z.
DOMAIN.
I LOOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.3%; Score 623.5; DB 1; Length 474; 34.9%; Pred. No. 7.3e-36; Pred. No. 7.3e-36; Ive 66; Mismatches 144; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOLIPID BINDING (PROBABLE)
C2 DOMAIN 1.
C2 DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF52A26EAF923F6F CRC64;
                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DGKGKKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 134 PO
135 474 CY
136 434 CY
206 236 CC
339 430 CZ
474 AA; 53278 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 DMEELTENAE----EGDEE--
                                                                                                                           EMBL, M55048; AAA28925.1; -. PIR, B39052; BMFFSY. HSSP, P21707; LBYN. FlyBase; FBgn0004242; syt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASPRRPIAQWHTLKD 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 DYPRRQIAKWHVLCD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Matches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
SYT7 HUMAN
ID SYT7 HUMAN
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TRANSMEM
DOMAIN
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402 AA.

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 -----SLISEMLMLSPGSEEDEAHEGCSRENLGRIQFSVGYNFQESTLILKIMKAQE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 RGRSEKKAIKLPAGGKAVNTAPVPGQTPHDESDRR----TEPRS----SVSDLVM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NSLETVGTPDSG
                                                                                                                                                                                                                                                                                                     MEDLINE-99277464; PubMed=9615227;
Cooper P.R., Nowak N.J., Higgins M.J., Church D.M., Shows T.B.;
"Transcript mapping of the human chromosome 11q12-q13.1 gene-rich region identifies several newly described conserved genes.";
Genomics 49:419-429(1998).
-!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of secretory vesicles through Ca(2+) and phospholipid binding to C2 domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis (By similarity).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC VESICLES (By similarity).
-!- TISSUE SPECIFICITY: Expressed in a variety of adult and fetal
                                                                                                                                                                              Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
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                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VESICULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1e-35;
nes 130;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-ERB-2003 (Rel. 41, Last annotation update)
Synaptotagmin VII (SytVII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2 DOMAIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 IITVSLSVTVVLCGLCHWCQRKLGKRYK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF038535; AAB92667.1; ALT_INIT.
HSSP; P21707; 1RSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEAR, PF00168; C2; 2.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPYOTAGMN.
SWART; SM00239; C2; 2.
PROSITE; PS00499; C2 DOMAIN 1; 2.
PROSITE; PS50004; C2 DOMAIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR001565; Synaptotagmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Repeat; Synapse.
DOMAIN 16 36 POTE
DOMAIN 37 402 CYTO
DOMAIN 136 238 C2 D
DOMAIN 267 370 C2 D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45561 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:11514; SYT7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KNEVK-----
                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                  NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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                                                                                                                                                                                                                                                                                                  337
LPAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALH 239
                                                                  219
                                                                                                                          299
                                                                                                                                                                                                                         TINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFV 359
                                                                                                                                                                                                                                                                                                                                                         419
                                                                                                                                                                                                                                                                                                                                                                     Aplysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia
                               SANSIIVNIIKARNEKAMDIGGISDPYVKVWEMYKDKRVEKKKTVTWKRNENENPENESFA
                                                                                                                                                                                                                                                                                                                                     FDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKW
                                                                                                           FILLSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitted (NOV-1993) to the EMBL/GenBank/DDBJ databases, FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS DURING TRAFFICKING OF SYNAPPICKING OF SYNAPPICKING OF SYNAPPICKING THE ACTIVE ZONE OF THE REQUIRES. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL BACKBONE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PHOSPHOLIPID BINDING (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM002399; C2 DOMAIN.
PROSITE; PS500499; C2 DOMAIN.
Transmembrane; Repeat; Synapse; Glycoprotein.
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000008; C2,
InterPro; IPR002149; LRI.
InterPro; IPR001565; Synaptotagmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U03125; AAA03567.1;
HSSP; P21707; 1RSY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
426
393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synaptotagmin (p65).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HQL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ganglion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURES.
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93
145
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P41823;
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TRANSMEM
DOMAIN
DOMAIN
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125
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                                                                                                                                                                                                                                                                                                                                                         DRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIK---RNVRKSSGRGELLISLCYQSTTN 302
                                                                                                                                                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                         362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 KLTVVILEAKNIKKONUGGESDPYVKIALIGGTKRIKKKKTTIKKNTINPYFNESFGFEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCEGLEDISVEFLVLDSERGSRNEVIGOLVLGAAAEGTGGEHWKEICDYPRRQIAKWHVL 422
                                                                                                                          65
                                                                                                                                             64 EIENLPIWAIVLIIAGSLLFLVCCVYCVCRRSCRKKKKKEGKKG-----LKGA----V
                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Homotetramer (Probable). Interacts with stonin 2.
-!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND CHROMAFIN GRANULES.
-!- DOMAIN: The first C2 domain mediates Ca(2+)-dependent phospholipid
                                                                                                                   EFDEIPT-VVGIFSAFGLVFTVSLFAWIC----CORKSSKSNKTPPYKFVHVLKGVDIYPE
                                                                                                                                                                         66 NINSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENATPKL
                                                                                                                                                                                                                                      126 FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDE
                                                                                                                                                                                                                                                                                              186 QSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSF
                                                                                                                                                                                                              ---MEDNEDA---
                                                                                                                                                                                                                                                                                                                TLTVVVJLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDI
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Adachi R., Teich A.H., Nigam R.;

"Genomic structure of the murine Syt2 gene.";

"Genomic teructure of to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS

-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS

DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE

SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT

REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The second C2 domain mediates interaction with Stonin
                                                                                           71;
                                                               426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95050743; PubMed=7961887;
Fukuda M., Aruga J., Niinobe M., Aimoto S., Mikoshiba K.;
"Inositol-1,3,4,5-terzakisphosphate binding to C2B domain
IP4BP/Symaptotagmin II.";
J. Biol. Chem. 269:29206-29211(1994).
                                                              Length
                                                                                         Indels
 C2 DOMAIN 1.
C2 DOMAIN 2.
2576B853DEEDEA85 CRC64;
                                                                                                                                                                                                        113 DLKSVQLLG----NSYKEKP-----DLDBLPVN---
                                                           ; Score 606.5; DB 1;
; Pred. No. 9.4e-35;
72; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
08-EEB-2003 (Rel. 41, Last annotation update)
Synaptotagmin II (SytII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
254 C2
389 C2
47459 MW;
                                                        27.6%;
36.0%;
                                                                                       151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
167 2
298 3
426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKBONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYTZ MOUSE
P46097;
                                                                                                                    10
                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
                                                         Query Match
Best Local
             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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STANDARD;
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           SYT2 RAT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 YPENLINSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLINGNFPKTNLKPGSPSDLENAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 PKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKKARGLPA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFDIPCEGLEDISVEFLVLDSERGSRNEVIGOLVLGAAAEGTGGEHWKEICDYPRRQIAK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 EFDEIP----TVVGIFSAFGLVFTVSLFA---WICCORKSSKSNKTPPYKFVHVLKGVDI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 LSFDRFSRDDIIGEVLIPLSGIEL----SEGKMLMNREIIKRNVRKSSGRGELLISLCYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 PTAGKUTVCILEAKNIKKONDVGGLSDPYVKIHLMQNGKRIKKKKTTVKKKTILNPYFNESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 MDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 STINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (POTENTIAL)
B4BD13FF70E0481B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ETGLTEG
                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOLIPID BINDING (PROBABLE)
C2 DOMAIN 1.
C2 DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 604.5; DB 1; Length 4; Pred. No. 1.3e-34; 63; Mismatches 127; Indels
                                                                                                                                EMBL; D37793; BAA07041.1; -
EMBL; D4757303; AAF68987.1; -
EMBL; AF257303; AAF68987.1; -
EMBL; AF257303; AAF68988.1; -
EMBL; AF257303; AAF68988.1; -
EMBL; AF257307; LBYN.

MGD; MGI:99666; Syt2.

RILCEPPO; IPR001149; LRI.

InterPro; IPR001149; LRI.

R Pfan; PF00168; C2; 2
R PRINTS; PR00369; C2DOMAIN.

R RNANTS; PR00399; SYNAPTOTAGNN.

R PROSITE; PS00499; C2_DOMAIN.1; 2.

R PROSITE; PS00494; C2_DOMAIN.1; 2.

R PROSITE; PS00494; C2_DOMAIN.1; 2.

R PROSITE; PS00494; C2_DOMAIN.1; 2.

R PROSITE; PS00496; C2_DOMAIN.1; 2.

R PROSITE; PS00496; C3_DOMAIN.1; 2.

R PROSITE; PS0044; C3_DOMAIN.1; 2.

R PROSITE; PS00496; C3_DOMAIN.1; 2.
 SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      C2 DOMAIN 2.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 -KNAMMKDMKGGODDDA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 47262 MW;
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35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 151; Conservative
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87
422
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245
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 266:13548-13552(1991).
-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EFDEIP----TVVGIFSAFGLVFTVSLFA---WICCORKSSKSNKTPPYKFVHVLKGVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elimitarity)
-!- SUBCELIGIARITY ENCATION: SYNAPTIC VESICLES AND CHROMAFFIN GRANULES
-!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN PHYLOGENETICALLY
OLDER BRAIN REGIONS SUCH AS THE SPINAL CORD, BRAIN STEM AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding.
-1- DOMAIN: The second C2 domain mediates interaction with Stonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homotetramer (Probable). Interacts with Stonin 2 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                            MEDLINE=91310620; PubMed=1856191;
Geppert M., Archer B.T. III, Suedhof T.C.;
"Synaptotagmin II. A novel differentially distributed form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.4%; Score 603.5; DB 1; Length 422; 35.6%; Pred. No. 1.5e-34; Indels 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHOLIPID BINDING (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, 92707; IBYN.

HSSP, 921707; IBYN.

InterPro; IPR000008; C2.

InterPro; IPR00149; LRI.

R InterPro; IPR001565; Synaptotagmin.

R PENNTS; PR00360; C220OMAIN.

R RRINTS; PR00399; SYNAPTOTAGMN.

R RRINT; SM00239; C22 2; 2.

R RROSITE; PS000499; C2 DOMAIN 1; 2.

RROSITE; PS50004; C2_DOMAIN 1; 2.

RROSITE; PS50004; C2_DOMAIN 2; 2.

KW Transmembrane; Repeat; Synapse; Glycoprotein.
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378 C2 DOMAIN 2.
32 N-LINKED (GLORAC. ) (P
47209 MW, D852AF5387E0C7FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (By similarity).
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. CYTOPLASMIC (POTENTIAL)
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last armotation update)
Synaptotagmin II (SytII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M64488; AAA63502.1; -.
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                                                                                                                                              Rattus norvegicus (Rat)
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136
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287
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422 AA;
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                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                 synaptotagmin.";
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InterPro; IPR001565; Synaptotagmin.
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                                      130
                                                                 182
                                                                                           171
                                                                                                                      242
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                                                                                                                                                                                                                         299 STINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELF 358
                                                                                                                                                                     LSFDRFSRDDIIGEVLIPLSGIEL----SEGKMLMNREIIKRNVRKSSGRGELLISLCYQ 298
                                                                                                                                                                                    230 YDFDRFSKHDIIGEVKVPMNIYDLGQPIEEWRDLQGGE--KEEPEK---LGDICTSLRIY 284
                                                                                                                                                                                                                                                             344
                                                                                                                                                                                                                                                                               359 VFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRQIAK 418
                                                                                                                                                                                                                                                                                                YPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENAT
                                                                                   ----EEKEPENLGKLOFSLDYDFQANQLTVGVLQAAELPA
                                                        PKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGLPA
                                                                                                               183 MDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTI
                                                                                                                              MEDLINE-91273991; PubMed-2054189;
Wendland B., Miller K.G., Schilling J., Scheller R.H.;
"Differential expression of the p65 gene family.";
Neuron 6:993-1007(1991).
-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE SYNAPSE: IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Discopyge ommata (Electric ray).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Torpediniformes, Narcinoidei, Narcinidae, Discopyge.
                                     ----ETGLTEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
-!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synaptotagmin C (Synaptic vesicle protein O-p65-C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         537 AA
                                - KNAMNMKDMKGGODDDDA
                                                                                      ----BGEGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  WHSL 408
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EMBL; M64277; AAA49229.1; PIR; JH0415; JH0415.

HSSP; P21707; 1RSY. InterPro; IPR000008; C2. InterPro; IPR002149; LRI

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171
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                                                                                                                                                                                                                                                                                   TRHIBIDISVSLLSVIVTFCGIVLLGVSLFVSWKLCWIPWRDKGLNPQRRDSQHH---PH 102
                                                                                                                                                                                                                                                                                                                      52 KFVH-----VLKGVDIYPENINSKKKFGADDKNEVKNKPAVPKNSIHLDLEKRDIN 102
                                                                                                                                                                                                                                                                                                                                                        ---- 135
                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                                                                                                                                                             313 ELQNRKLHFSVYDFDRFSRHDLIGQVVLDNLLEFSDFSEDTTIW-RDILEATSEKAD-LG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 PNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEIC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 INPVZNEALVEDIENENMEHVNVIIAVMDXDCIGHNEVIGMCRVGNATDGPGREHWNEML 490
                                                                                                                                                                                                                                                                                                                                                                                                                                 TPKLFLEGEKE-----SVSPESLKSSTSLTSEEKQEKL--GTLFFSLEYNFERKAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 QIQELALHFTILSFDRFSRDDIIGEVLIP--LSGIELSEGKMLMNREIIKRNVRKSSGRG
                                                                                                                                                                                                                                                                         -----ORKSSKSNKTPPY
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                                                                                                                                                                                                                                               Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                             Indels 111;
                                                                                                                               CYTOPLASMIC (POTENTIAL). PHOSPHOLIPID BINDING (PROBABLE).
                                                                                                                                                                                                             27.0%; Score 594.5; DB 1; Length 537; 31.5%; Pred. No. 8.7e-34;
                                                                                                                                                        C2 DOMAIN 1.
C2 DOMAIN 2.
2792F910CFBCE682 CRC64;
GNFPKTNLK-----PGSPSDL----EN-----
                                                                                                                                                                                                                                           88; Mismatches 140;
                                                                                                                                                                                                                                                                  6 TSREEFDEIPTVVGIFSAF-GLVFT-VSLF-AWICC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYT1_CAEEL STANDARD; PRT; 441 AA. P34693; 01-FBE1994 (Rel. 28, Last sequence update) 01-FBE 1994 (Rel. 28, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         103 QHLHHHHSHFTDLTVERVDCGPE-
                                                                                                                                                                                   61300 MW;
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537
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SNT-1 OR F31E8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                        Matches 156;
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                                                                                                                                                                                   SEQUENCE
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                     246 IYDFDRFSKHDQIGQVLIPLGKIDL--GAVIBEWKDIAPPPDDKEAEKS--LGDICFSLR 301
                                                                                                                                                                                           297 YQSTINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNE
                                                                                                            357 LFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGOLVLGAAAEGTGGE--HWKEICDYPRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel seizure-induced synaptotagmin gene identified by differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 94:2638-2641(1997).

-!- FUNCTION: May be involved in Ca(2+)-dependent exocytosis of secretory vesicles through Ca(2+) and phospholipid binding to the C2 domain or may serve as Ca(2+) sensors in the process of vesicular trafficking and exocytosis (By similarity).
-!- SUBGUNIT: Homodimer. Can also form heterodimer (By similarity).
-!- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SYNAPTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Babity J.M., Armstrong J.N., Plumier J.C., Currie R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VESICLES (By similarity).
--- SIMILARITY: Contains 2 C2 domains.
--- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VESICULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Synaptotagmin X (SytX) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                             498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P21707; 1BYN.
InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR001565; Synaptotagmin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
MEDLINE=97226006; PubMed=9122248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane, Repeat; Synapse.
DOMAIN 1 55 VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfan; PF00168; C2; 2. PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U85513; AAB51686.1; -. PIR; PC6300; PC6300.
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                        415 QIAKWHVL 422
                                                                                                                                                                                                                                                                                               420 PİAQWHTL 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robertson H.A.;
                                                                                                                                                                                                             362
                                                                                                                                                                                                                                                                                                                                                                                                         SYTA RAT
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                                                                                                                                                                                                        원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 AMDEQSMISDPYIKWTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 KKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPK-----TNLKPGSPSDLENAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 GMD-MSGISDPYVKLYLLPEKKKKVETKVHRKILNPVENETFIF-KVAFNEITAKTLVFA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 ILSFDRFSRDDIIGEVLIPLSGIELSEGKMLANREII-----KRNVRKSSGRGELLISLC 296
                                                                                                                                                               Du Z.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY HAVE A REGULATORY ROLLE IN THE MEMBRANE INTERACTIONS
DURING TRAFFICKING OF SYMAPTIC VESICLES AT THE ACTIVE ZONE OF THE SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL BACKBONE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
                                                                                                                                                                                                                                                                                                                                                                               SYMAPSES AND APPEARS TO BE ASSOCIATED WITH SYMAPTIC VESICLES.
ALSO FOUND IN SOME NONNEURONAL SECRETORY STRUCTURES.
DISEASE: MUTANTS EXHIBIT SEVERE BEHAVIORAL ABNORMALITIES THAT ARE SEVER LOCOMOTION, PERILING, AND DEFECATION DEFECTS.
STMILARITY: Contains 2 C2 domains.
SIMILARITY: BELONGS TO THE SYNAPTORGMIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKLFGKKRHGE-KNK-------KGGLKGFFGKGDDVVDGKNIQ-GMAQDLBELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 PKLFLEGEKESVSPESLKSSTSLTSEEKQE-KLGTLFFSLEYNFERKAFVVNIKEARGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: LOCALIZED TO REGIONS KNOWN TO BE RICH IN
MEDLINE=93313960; PubMed=8391930; Nonet M.L., Grundahl K., Meyer B.J., Rand J.B.; "Synaptic function is impaired but not eliminated in C. elegans mutants lacking synaptotagmin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.0%; Score 594; DB 1; Length 441; 40.2%; Pred. No. 7.2e-34; ive 57; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F8D174337EB472DB CRC64;
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C2 DOMAIN 2
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InterPro, IPR002149; LRI.
InterPro, IPR001565; Synaptotagmin.
Pfam; PF00168; C2; 2.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR0399; SYNAPTOTAGMN.
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                                                                                        Cell 73:1291-1305(1993).
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262
397
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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16;
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111 EEKKEVEENEKPAPK-AIEPAIKISHTSPDIPAEVQTALKEHLIKHARVQRQTTDPTSSS 169
                                                                                                                                                                                                                                                                                                                                                             151 QEKLGTLFPSLEYNPERKAFVVNIKEARGLPAMDEQSWISDPYIKWTILPEKKHKVKTRV 210
229 VKTCGKLNFALQYDYENBLLVVKIIKALDLPAKDSTG-TSDPYVKIYLLPDRKKKFQTRV 287
                                                                                                                                                                                                                              ----PGSPS 116
                                                                                                                                                                                                                                                                                           -----DLENATPKLFLEGEKES----VSPESLKSSTSLTSE----EK 150
                                                                                                                                                                                                                                                                                                                       170 RHNSFRRHLPRQMNVSSVDFSMGTEPVLQRGETRTSIGRIKPELYKQK-SVDSEGNRKDD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                   211 LRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 HRKTLMPLFDELFQF-PVVYDQLSNRKLHFSIYDFDRFSRHDMIGEVILD----NLFEVS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 MIMNREIIKRNVR----KSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPY 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 DLSREATVWKDIHCATTESMDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDPY 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 VKVSLMCEGRRLKKRKTTTKKNTLNPVYNEALIFDIPPENVDQVSLCIAVMDYDRVGHNE 462
                                                                                                                                           20 IFSAFGL-VFTVSLFA-WICCORKSSKSNKTPPYKFVHVLKGVDIYPENLNS--KKKFGA 75
                                                                                                                   70; Gaps
                                                                                Length 498;
                                                                     Query Match 26.9%; Score 592; DB 1; Length 498
Best Local Similarity 34.6%; Pred. No. 1.2e-33;
Matches 158; Conservative 72; Mismatches 156; Indels
                                      56411 MW; 620BD7CD372057DE CRC64;
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     C2 DOMAIN 2.
     365 4
498 4
498 AA;
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Search completed: February 20, 2004, 13:13:18 Job time: 18 secs

Q99p37 rattus norv Q99p35 rattus norv Q99p35 rattus norv Q99p34 rattus norv Q99p38 rattus norv Q99p38 rattus norv Q90mf3 manduca sex Q8nbe5 homo sapien Q870e1 mus musculu Q8746 rattus norv Q8n910 homo sapien Q970n8 mus musculu Q970n8 mus musculu Q925b8 rattus norv Q925p7 caenorhabdi Q925c0 rattus norv Q97cn9 mus musculu Q825c0 rattus norv Q97cn9 mus musculu Q825c1 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv Q925p7 rattus norv

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ein - pro Boore:	Scoring table: BLOSUM62  Gapop 10.0 , Gapext 0.5  Searched: 830525 segs, 258052604 residues  Total number of hits satisfying chosen parameters: 830525  Minimum DB seg length: 0  Maximum DB seg length: 2000000000  Post-processing: Minimum Match 0%  Maximum Match 100%  Database: SPTEMBL 23:**	2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_human:* 6: sp_mammal:* 7: sp_mhc:* 9: sp_phage:* 10: sp_plant:* 11: sp_codent:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:* 15: sp_ratrus:* 16: sp_acteriap:* 17: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 17: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_arc	V Length DB + 425 111 4 4 4 4 5 4 1 4 4 5 4 4 5 4 4 5 4 4 4 5 4 4 4 4

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DIPCESLEEISVEFLVLDSERGSRNEVIGRLVLGATAEGSGGGHWKEICDFPRRQIAKWH 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97306341; PubMed=9162066;
Von Poser C., Ichtchenko K., Shao X., Rizo J., Sudhof T.C.;
"The evolutionary pressure to inactivate. A subclass of synaptotagmins with an amino acid substitution that abolishes Ca2+ binding.";
                  TNTLTVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVF
                                                                                         DIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEJCDYPRRQIAKWH
                                    59 GVDIYPENLINSKKKFGADDKNEVKNKPAVPKNSLHLDLEK-----RDLNGNFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GISİYPETLENKKKIIKVRRDKDGSHRESGRGNLLVNAESGLLSHDRDPRGPSPASCIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 NEERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETF
                                                                                                                                                                                                                                                                                                                                                                                                                                               natus.
Bukaryota, Metazoa, Kat,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LPIKRDYGEELRSPMTSLTP----GESKPTSP-----SSPEEDVMLGSLTFSVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 TFYGIPYSQLQDLVLHFLVLSFDRFSRDDVIGEVWVPLAGVDPSTGKVQLTRDIIKRNIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.7%; Score 1160.5; DB 11; Length 430; 51.7%; Pred. No. 3.7e-77; 1.1ve 77; Mismatches 104; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Shin O.-H., von Poser C., Ichtchenko K., Shao X.,
Sudhof T.C.;
                                                                                                                                                                                                                                                                                                                    430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: CONTAINS 2 C2 DOMAINS BMBL; AR7356560.1; -. INCEPPC; IPR000008; C2.
                                                                                                                                                                                                                                                                                                                                                           Created)
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ATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGL 180
                            121 VTPKLFTETEKBANSPESLKSSTSLTSEEKQEKLGTLFLSLEYNFEKKAFVVNIKEAQGL 180
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                                                                                                      DIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKWH
                                                                             PAMDEQSMTSDPYIKWTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHF
                                                                                                                                                                                                                                                               DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLEN
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SEQUENCE FROM N.A.
STRAIN-C57BL/61; ITSSUE-Cortex;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of the constant of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of the consecution of t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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90.6%; Score 1994; DB 11; Length 425;
Best Local Similarity 89.6%; Pred. No. 2.2e-138;
Matches 381; Conservative 21; Mismatches 23; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK043985; BAC31726.1; -
SEQUENCE 425 AA; 47658 MW; 60011E4F23A7F6EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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421 MLCDG
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349 TPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGA-AAEGTGGEHWKE 407
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC039205; AAH39205.1; -.
SEOUENCE 431 AA; 48348 MW; B2EB06B250DC9A68 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Q8QZS8;
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RA 150GBICE FROM N.A.
RA 150GBI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA 150GBI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA 150GBI T., Ota T., Hayashi K., Sugiyama T., Sudo H.,
RA 170GBI M., Hosoiri T., Kaku Y., Kadaira H., Kondo H.,
RA 170GBI M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA 170GBI M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA 270GBI M., Chiba Y., Maxamatsu A., Nakamura Y., Rayanati K., Masuho Y.,
RA 170GBI M. 170GBI T.,
RT 170GBI M. 170GBI T.,
RT 170GBI M. 170GBI T.,
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    343 THVKKCTPNAVFNELFVFDIPCEGLEDISVEFLYLDSERGSRNEVIGQLVLGAAAEGT-G 401
                            59 GVDIYPENLNSKKKF----GADDKNEVKNKPAVPKNSIHLDLEKRDLNGNFPKTNLKPG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 FVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPARDETFTRYGIP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 YTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRG 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAEITNIRESFDVSPVVAGLIGASVLVVCVSVTVFVWSCCHQQAEKKHKSPPYKFIHMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||| |::||||
|GISIYPETLSNKKKIIKVRRDKDGPGREGGRRNLLVDAARAGLLSRD-----KDPRGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypotherical protein FLJ14634.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.7%; Score 1159; DB 4;
Best Local Similarity 52.4%; Pred. No. 4.8e-77;
Matches 229; Conservative 77; Mismatches 111;
                                                                                                                                                                                                                                    431 AA
                                                                                  402 GEHWKEICDYPRRQIAKWHVLCD 424
                                                                                                        407 AEHWREVCESPRKPVAKWHSLSE 429
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                              TLTVVVLKARHLPKSDVSGLS-DPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFD
                                                                                                                                                                                                                                                                                                                     183 MDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPCEGLEDISVEFLVLDSERGSRNEVIGOLVLGAAAEGT-GGEHWKEICDYPRRQIAKWH
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Chavez C., Dorsett V., Kronmiller B., Li P., Liao G.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
             Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                              2;
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                               39.7%; Score 874; DB 11; Length 245; 65.2%; Pred. No. 2e-56;
                                                                                                                                                                                                                                                                Score 8,2, Pred. No. 2e-56;
Pred. No. 2e-56;
                                                                                              Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
EMBL; BC025207; AAH25207.1; -.
INTERPRO; IPR000008; C2.
InterPro; IPR002149; LRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Celliker S.;
Celliker S.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: CONTAINS. 2 C2 DOMAINS.
EMBL, AYO71620; AAL49242.1;
-! PlyBase; FBGn0028400; SytiV.
InterPro; IPR002008; C2.
InterPro; IRR002149; IRI.
Pfam; PF00168; C2; 2.
                                                                                                                                                                                   PFam; PF00168; C2; 2.
SMART; SM00239; C2; 2.
PROSITE; PS50004; C2 DOMAIN 2; 2.
SEQUENCE 245 AA; 28092 MW; 65B2BFD155D5865F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                           46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly)
Similar to synaptotagmin IV.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                          Local Similarity 65.2
les 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                    SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLCD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 SLSE 244
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                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                 125 NOLTVVDGNGLKHSLHNSLHHSPVETIANGSVTITLDDHSLTNGKELTVTDQYGKLGTIY 184
                                                                                                                                                                54
                                                                                                                                                                                             71
                                                                                                                                                                           104 N----FPKTNLKPGSPSDLENATPKLFLEGEKE-SVSPESLKSSTSLTSEEKQEKLGTLF
                                                                                                                                                                                                                                                                                                                                                                   159 FSLEYNFERKAFVVNIKEARGLPAMDEQSMT-------SDPYIKMTILPEKKH
                                                                                                                                                                                                                                                                                                                                                                                                            205 KVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIJGEVLIPLSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                245 KVKTRVVRNTRNPVYDEDFTFYGINMNDLQNMSLHFVILSFDRYSRDDVIGEVVCPLTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 E---LSEGKMLMNREIIKRNVR-KSSGRGELLISLCYQSTTNTLTVVVJLKARHLPKSDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 GLADPYVKIYLLYNGQRIAKKKTHVKKRTLSPVFNESFAFDIPAAEGAGASLEGVSLELM
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Littleton J.T., Sereno T.L., Rubin G.M., Chapman E.R., Ganetzky B., "Synaptic function modulated by changes in the ratio of synaptotagmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q.; Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                                70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Arthropoda, Hexpoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                  Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 VLDSERGSRNEVIGQLVLGAA-AEGTGGEHWKEICDYPRRQIAKWHVL
                                                                                         34.5%; Score 759; DB 5; Length 47
38.2%; Pred. No. 1.3e-47;
ive 82; Mismatches 137; Indels
                                                                                                                                                          14 IPTVVGIFSAFGLVFTVSLFAWICCQ-----RKSSKSNKTPPYKFV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 GLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIP-CEG
SWART; SM00239; C2; 2.

PROSITE; PS00499; C2 DOWALN 1; 1.

PROSITE; PS50004; C2 DOWALN 2; 2.

474 AA; 52217 MW; 83853EF326622044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                     55 -HVLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrimBirel. 13, Created) 01-WAY-2000 (TrimBirel. 13, Last seq 01-WAR-2003 (TrimBirel. 23, Last ann
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MEDLINE=99394599; PubMed=10466723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein).
                                                                                                                           Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 400:757-760(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synaptotagmin IV (SYTIV SYTIV OR CG10047.
                                                                                                             Similarity
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                                                                                             Query Match
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J. Brokstein P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier R., Chaldra I., R. Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., M., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., M., Doubin K.J., Evangeliste A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Bodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Borsen C., Ferriacz C., Ferriacz S., Fleischmann W., R.A. Harvey D., Haiman T.J., Hernandez J.R., Houck J., Harvey D., Haiman T.J., Hernandez J.R., Houck J., Alalai M., Kalush P., Karpen G.H., Ke Z., Kenison J.B., Ketchum K.A., Jalai M., Kalush P., Karpen G.H., Ke Z., Kenison D., Harris M., Alalai M., Kalush P., Karpen G.H., Ke Z., Kenison D., Harris M., Matteri B.B., McIntosh T.C., McIrach M.P., Morberson D., Merkulov G., Milshina N.V., Modarry C., Morris J., Morberson D., Merkulov G., Milshina N.V., Modarry C., Morris J., Morberson D., Nobleson D.L., Rolson D.R., Nelson K., Sunder S., Pollard J., Puri V., Reese M.G., Shen H., Shirk B.C., Siden-Kamegon K., Sauders R.D., Puri V., Smith T., Shangson M., Stupski M.P., Smith T., Shangson M., Stupski M.P., Smith T., Shangson M., Stupski M.P., Smith H.O., The Grang S.A., Wallerson S.A., Wallerson S.A., Wallerson S., Zaveri J.S., Zhao W., Zhong S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho S., Zho 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 IPTVVGIFSAFGLVFTVSLFAWICCQ-----RKSSKSNKTPPYKFV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMANIS, ENVOLSS, C2; 2.
SMARI; SM00239; C2 DOMAIN 1; 1.
PROSITE; PS50004; C2 DOMAIN 2; 2.
PROSITE; P4 AA; 52229 MM; 83800ACDD66B2BB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR001565; Synaptotagmin.
Pfam; PF00168; C2; 2.
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PRINTS; PR00399; SYNAPTOTAGMN.
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FlyBase; FBgn0028400; SytIV.
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321 GLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIP-CEG----LEDISVBFL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GIFSAFGLVFTVSLFAWICCORKSSKSNKTPPYKFVHVLKGVDIYPENLNSKKKFGADDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73;
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                                                                                                                                                                                                      376 VLDSERGSRNEVIGQLVLGAA-AEGTGGEHWKEICDYPRRQIAKWHVL 422
                                                                                                                                                                                                                                           29.3%; Score 645.5; DB 5; Length 357; 37.8%; Pred. No. 1.9e-39; ive 63; Mismatches 119; Indels 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Katsuyama Y., Matsumoto J., Okamura Y.;
"Regulation of synaptotagmin gene in ascidian embryo.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
EMBL; AB044144; BAB18864.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synaptotagmin.
Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8D21585F00C045E1 CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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Best Local Similarity 37.8%
Matches 155; Conservative
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70 KKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENATPKLFLEG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Optic lobe;
Mischiba K., Fukuda M., Moreira J.E., Lewis F.M.T., Sugimori M.,
Niinobe M., Lilinas R.,
"Role of the C2A domain of synaptotagmin in transmitter release as determined by specific antibody injection into the squid giant synapse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 EKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 SDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 -----KDGKKGLKGA------VDLKGVQLLGNSIKEKVQP----DLEEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGIGGEHWKEICDYPRRQIAKWHVL 422
                                                                                                                                                                                                                                                                                                                                                                                            Loligo paaleii (Longfin squid).
Eukaryota, Metazoa, Mollusca, Cephalopoda, Coleoidea, Neocoleoidea,
Decapodiformes, Loliginidae, Loligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.5%; Score 627; DB 5; Length 42 34.6%; Pred. No. 5.5e-38; ive 75; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00499; C2 DOWAIN 1; 2.
PROSITE; PS50004; C2 DOMAIN 2; 2.
SEQUENCE 424 AA; 47656 MW; F9733D3B10CFF3C0 CRC64;
                                                                                                                                                                                                                                                                                                     01, Created)
01, Last sequence update)
23, Last annotation update)
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59 ELEKLPIWAIILICAGVLLFLVCGTYCCCKRICRRGK.
                                                                                                                                                                                                                                                            424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR001565; Synaptotagmin.
Pfam; PF00168; C2; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 144; Conservative
                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel.
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                                                                                                                                       401
                                                                                       420 HVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6621;
                                                                                                                                                                                                                                                                                                                                                                         Synaptotagmin.
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                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 LFLEGEKESVSPESLKSSTSLTSEE-----KQEKLGTLFFSLEYNFERKAFVVNIKEARG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LPAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALH 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 FDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKW 419
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Intestine,
MEDLINE=95312080; PubMed=7791877;
Li C., Ullrich B., Zhang J.Z., Anderson R.G., Brose N., Sudhof T.C.;
"Ca(2+)-dependent and -independent activities of neural and non-neural
                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SLTSEMLMLSPGSEEDEAHEGCSRENLGRLQFSVGYNFQESTLTVKVMKAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 FILLSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 VFTVSL-----FAWIC--CORKSSKSNKTPPYKFVHVLKGVDIYPENLNSKKKFGADD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NSLETVGTPDSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugita S., Han W., Butz S., Fernandez-Chacon R., Lao Y., Sudhof T.C "Synaptotagmin VII as a plasma membrane Ca2+ sensorin exocytosis."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
TVLDYDRMGKNDVIGRLILG--CNGTGAELRHWSDMLASPRRPIAQWHTL 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.5%; Score 627.5; DB 11; Length 403; 36.2%; Pred. No. 4.7e-38; ative 72; Mismatches 127; Indels 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00360; C2DOMAIN.

PRINTS; PR00399; SYNAPTOTAGMN.

SMART; SM00239; C2; 2; 2; PROSITE; PS00499; C2 DOMAIN 1; 2.

PROSITE; PS50004; C2 DOMAIN 2; 2.

SEQUENCE 403 AA; 45482 MW; 3153FD7FCIDBEBEFB CRC64;
                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Synaptotagmin VII (Synaptotagmin VIIS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 IITVSLSVTIVLCGLCHWCORKLGKRYK------
                                                                                                                         403 AA
                                                                                                                                                                       Created)
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HSSP; P21707; 1RSY.
InterPro; IPR000008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR0011655; Synaptotagmin.
Pfam; PF00168; C2; 2.
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                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                01-NOV-1996
01-NOV-1996
01-MAR-2003
  303
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                                                                      RESULT 10
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76F3A34EEABE875B CRC64;

53260 MW;

474 AA;

SEQUENCE

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ramantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Genardides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Randon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Randon R.C., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G., Battle R.M. Bast A. Baxendale J., Baytaktaroglu L., Beasley E.M., Ballew R.M. Bast A., Baxendale J., Baytaktaroglu L., Beasley E.M., Buttis V.C., Busam D.A., Butle J., Baytaktaroglu L., Beasley E.M., Buttis V.C., Cabusm D.A., Butle C., Davenpolt L., Bolchakov S., Buttis R.B., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M., Cherry J.M., Candey S., Dalkhe C., Davenpolt L.B., Davies P., Buttis R., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P., Buttis N.J., Evangelista C.C., Ferraz C., Ferriera S., Punkov B.C., Dunn P., Buttis N.J., Barvey D., Heiman T.J., Hernandez J.R., Houck J., Rallen R., Gabriellan A.E., Gabriel W., Gabriellan A.E., Gabriel W., Gabriellan A.E., Gabriel C., Karte C., Karvitz S., Mulp D., Lai Z., Liang Y., Lin X., Alland B.B., Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nattei B., McIntosh T.C., McIeod M.P., Marzhy D.M., Nelson D.L., Raken R.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Raken R.M., Modage T., Worley K.C., Wu D., Yang S., Yao Q.A., Shier K., Sheniston R.A., Wassarman D.A., Wassarman D.A., Wang K., Wang X., Wang X., Wang X., Wassarman D.A., Weinfiscon M., Strong R., Shier E., Spradling A.C., Stapleton M., Strong R., Smith T., Raben S., Pollow W., Shork W., Wang X., Wang X., Wang X., Wang S., Wang 362 IQKVSLYVIVUDXDRIGTSEPIGRTFLGCNSTGTGLRHWSDMLANPRRPVAQWHTL 417 Drosophila melanogaster (Fruit fly). Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 474 AA Science 287:2185-2195(2000). -!- SIMILARITY: CONTAINS 2 C2 DOMAINS. EMBL; AE003582; AAF51205.1; -. PRT; HSSP; P21707; 1BRN.
FlyBase; FBGD0004242; syt.
InterPro; IPR00008; C2.
InterPro; IPR002149; LRI.
InterPro; IPR002149; LRI.
Flam; PF00168; C2; 2. MEDLINE=20196006; PubMed=10731132; PROSITE; PS00499; C2 DOMAIN 1; 2. PROSITE; PS50004; C2 DOMAIN 2; 2. PRINTS; PR00360; C2DOMAIN. PRINTS; PR00399; SYNAPTOTAGMN PRELIMINARY; SMART; SM00239; C2; 2. SEQUENCE FROM N.A. NCBI TaxID=7227; STRAIN=BERKELEY; SYT protein. SYT OR CG3139. Q9VQG7 RESULT 12 Q9VQG7

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6
                                                                                                            144
                                                                                                                                                            145 -----DGKGKKG------VDMKSVQLLGSAYKEKVQP 170
                                                                                                                                                                                                          113 GSPSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVV 172
                                                                                                                                                                                                                                                                                                   212 TVIQAEELPALD-MGGTSDPYVKVYLLPDKKKKFETKVHRKTLSPVFNETFTSKSLPYAD 270
                                                                                                                                                                                                                                                                                                                                                                     271 AMNKTLVFAIFDFDRFSKHDQIGEVKVPLCTIDLAQ-TIEEWRDLV--SVEGEGGGEKLG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 PNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEIC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
                                                                       ----GIFSAFGLVFTVSLFAWICCORKSSKSNKTPPYK 52
                                                                                                     88 PVIKKIEHVGEVVTEVIAERTGLPTWGVVAIIILVFLVVFGIIFFCVRRFLKKRRTK---
                                                                                                                                       53 FVHVLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKP
                                                                                                                                                                                                                                                                              173 NIKBARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQ
                                                                                                                                                                                                                                                                                                                                               233 IQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGR---G
                                                                                                                                                                                                                                                                                                                                                                                                                     290 ELLISLCYQSTINTLITVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                          388 INPXYNESFSFEVPFEQIQKICLVVTVVDYDRIGTSEPIGRCILGCMGTGTELRHWSDML
                                                                                                                                                                                                                                                 ----DKQSEQKLGRLNFKLEYDFNSNSLAV
                                     Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
 ; Score 622.5; DB 5; Length 474;
; Pred. No. 1.4e-37;
67; Mismatches 144; Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.2%; Score 621.5; DB 11; Length 447; Best Local Similarity 34.6%; Pred. No. 1.5e-37; Matches 156; Conservative 76; Mismatches 136; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 447 AA; 50671 MW; C1968D5EAABF07B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                              171 DMEELTENAE-----EGDEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BALB/c; TISSUE-Brain;
MEDLINE-22067076; PubMed=12071850;
                                                                     3 PITTSREEFDEIPTVV----
   28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 DYPRROIAKWHVLCD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             448 ASPRRPIAOWHTLKD 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Brain;
                               Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synaptotagmin VIIbeta.
SYT VIIBETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                   Similarity
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Query Match
Best Local 8
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27 VFTVSL----FAWIC--CQRKSSKSNKTPPYKFVHVLKGVDIYPENLNSKKKFGADDKN 79

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Q9VQG8
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                                                                                     --PK---TNLKPGSPSDLENATPKL 125
                                                                                                           118 PAGGKAVNTAPVPGQTPHDESDRRTETRSSVSDLVNSLTSEMLMLSPGSBEDEAHEGCSR 177
                                                                                                                                                                                                                                                                                                                           EKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVL 211
                                                                                                                                                                                                                                                                                                                                                                                                   212 RKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIBLSEGKM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 LMNREIIKRNVRKSSGRGELLISLCYQSTINTLTVVVLKARHLPKSDVSGLSDPYVKVNL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 YHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQL 391
                                                                                                                                                                                                    ----KQ 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354
        295 QTFWKDLKPCSDGSGSRGELLLSLCYNPSANSIIVNIIKARNLKAMDIGGTSDPYVKVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 MYKDKRVEKKKTVTKKRNLNPIFNESFAFDIPTEKLRETIIIITVMDKDKLSRNDVIGKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loligo pealeii (Longfin squid).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Loliginidae; Loligo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Augustine G.J.;
"Inhibition of neurotransmitter release by C2-domain peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93247639; PubMed=8097867;
Bommert K., Charlton M.P., De Bello W., Chin G., Betz H.,
Augustine G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.2%; Score 621; DB 5; Length 40 35.6%; Pred. No. 1.4e-37; rive 71; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45434 MW; 74ADF87A0B5FD838 CRC64;
                                                                                                                                                                                126 FLEGEKESVSP------ESLKSS----TSLTSEE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01, Last sequence update)
23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : :|||:: ||: 415 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445 | 445
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Nature 363:163-164(1993)
-!- SINITARITY: CONTAINS 2 C2 DOMAINS.
BMBL; X72386; CAA51079.1; -.
HSSP; P21707; 1BYN.
InterPro; IPR001008; C2.
InterPro; IPR001068; C2.
InterPro; IPR001565; Synaptotagmin.
PF00168; C2; 2.
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: |||| : |||| | 23 IITVSLSVTIVLCGLCHWCQRRLGKRYK-
                                                                             80 EVKNKPAVPKNSLHLDLEKRDLNGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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PROSITE; PS00499; C2_DOMAIN_1; 2.
PROSITE; PS50004; C2_DOMAIN_2; 2.
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PRINTS; PR00399; SYNAPTOTAGMN.
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Best Local Similarity 35.64
Matches 149; Conservative
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01-MAR-2003 (TrEMBLrel.
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10 EFDEIPTVVGIFSAFGLVFTVSLFAMICCQ----RKSSKSNKTPPYKFVHVLKGVDIYPEN

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RA MGDIANE=2UL950U05; FUDNEG=1U731132;

RA AGEMEN M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA AMMARTIGES P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Cann P., Harris M.,

RA Hostin D., Houston K.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mopherson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny B.M., Nelson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny B.M., Nelson D.L.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
                                                                                                                           186
                                                                                                                                                  246
                                                                                                                                                                                                                        RFSRDDIIGEVLIPLSGIELSEGKMLMN-REIIK--RNVRKSSGRGELLISLCYQSTTNT 303
                                                                                                                                                                                                                                                                                                                                                            LTVVVLLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIP 363
                                                                                                                                                                                                                                                                                                                                                                                     CEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKWHVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 INSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENATPKLF
                                                                                                                 127 LEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQ
40 ELEKLPIWAIILICAGVLLFLVCGTYCCCKRICRRGKKDGKKGLKGAVDLRGVQLL---
                                                                                    --MEDNEDA----
                                                                                                                                                                                                 SMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                              ---GNSIKEKP-----DLEELPMN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 AA
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MEDLINE=20196006; PubMed=10731132;
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22,
23,
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01-MAY-2000 (TrEMBLrel. 1:
01-OCT-2002 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
CG3139 protein.
SYT OR CG3139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang San. Massarman D.A., Weinstock G.M., Weissenbach J., Valliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O., The genome sequence of Drosophila melanogaster.", Science 287:2185-2195(2000) RAPARA RA

SEQUENCE FROM N.A.

Genliker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Genliker S.E., Adams M.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Gorzler S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson R.A., Nunco J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Moshrefi A.,
RA Phouanemavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
R. Sequencing of Drosophila melanogaster genome.", C., Rubin G.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Supmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A.

EMBL/GenBank/DDBJ databases C2 DOMAINS Submitted (SEP-2002) to the -!- SIMILARITY: CONTAINS 2 (EMBL; AE003582; AAF51206.2; FlyBase; FBGn0004242; syt. NO STUDENT STREE

InterPro; IPR000088; C2. InterPro; IPR002149; LRI. InterPro; IPR001565; Synaptotagmin.

Pfam; PF00168; C2; 2.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 2.

40BB77BB9D468FCA CRC64; PROSITE; PS00499; C2 DOMAIN 1; 2. PROSITE; PS50004; C2 DOMAIN 2; 2. SEQUENCE 472 AA; 53032 MW; 40

53 FVHVLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKP 112 88 PVIKKIEHVGEVVTEVIAERTGLPTWGVVAIIILVFLVVFGIIFFCVRRFLKKRRTKDGK PITTSREEFDEIPTVV-----GIFSAFGLVFTVSLFAWICCORKSSKSNKTPPYK 75; 28.1%; Score 617.5; DB 5; Length 472; 35.6%; Pred. No. 3.1e-37; ive 65; Mismatches 140; Indels 75, Query Match
28.1%;
Best Local Similarity 35.6%;
Matches 155; Conservative 6 m

113 GSPSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVV 172

148 ---GKKGVD-----DMKSVQLLG----SAYKEKP-----DMEEL-

:::||| | | |||:| ---DKQSEQKLGRLNFKLEYDFNSNSLAV 209 289 173 NIKEARGLPAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQ 232 290 ELLISLCYQSTINTLITVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCT 349 385 350 PNAVENELFVEDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGIGGEHWKEIC 409 386 LNPYYNBSFSFBYPFEQIQKICLVVTVVDYDRIGTSEPIGRCILGCMGTGTELRHWSDML 445 233 IQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKWLMNREIIKRNVRKSSGR---G 269 AMNKTLVFAIFDFDRFSKHDQIGEVKVFLCTIDLAQ-TIEEWRDLV--SVEGEGGGEKLG 410 DYPRRQIAKWHVLCD 424 446 ASPRRPIAOWHTLKD 460 326 à g ð 엄 ਨੋ g 8 g à

completed: February 20, 2004, 13:14:11 41 secs Search comp Job time :

	Ltd.
5.1.6	Compugen
version	- 2004
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OM protein - protein search, using sw model

February 20, 2004, 13:11:10 ; Search time 20 Seconds (without alignments) 2043.584 Million cell updates/sec Run on:

US-09-680-121C-2 Perfect score: Title:

Sequence:

1 MAPITTSREEFDEIPTVVGI......KBICDYPRRQIAKWHVLCDG

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

synaptotagmin o-p6 synaptotagmin p65 synaptotagmin p65 synaptogamin o-p65 synaptotagmin - fr synaptotagmin - lo synaptotagmin II -cellutagmin I sytv synaptogamin o-p65 synaptotagmin IV synaptotagmin II -Synaptotagmin X synaptotagmin V -hypothetical prote synaptotagmin I synaptotagmin V double C2 protein Bynaptotagmin
B/K protein -1ypothetical rabphilin-3A rabphilin-3A Description SUMMARIES S58399 JH0415 A40707 PC6300 151210 TH0414 159387 S58402 T28967 A53563 S33318 BMRT2Y 158166 T32059 JC2473 T33485 S58400 BMFFSY BMHU1Y A45486 JH0413 S09595 JC4921 T16355 A48097 159355 H Length Query Match 2006 627.5 623.5 623.5 603.5 603.5 603.5 594.5 592 Score 579.5 577 574.5 573.5 573.5 544.5 520 474 430.5 415 416 394.5 393.5 390.5 384.5 377.5 Result

synaptotagmin VIII hypothetical prote	acuble Cz protein, hypothetical prote	processing proce	protein kinase C ( protein kinase C (	hypothetical prote protein kinase C (	hypothetical prote	Synaptotagmin VIII	Ins P4-binding pro
S58401 S44644	T24770 T00634	KIBOGC	D24664	KIRTGC	T00332	S58403 KIBOC	558888
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355 1021 387	448	682	697	697	1212	137	829
16.4 15.1 14.7	0.8	8.5	88.1	. 6. 6. 1 - 1 - 1	9.7	7.5	7.4
361.5 332 323	217.5	179.5	178.5	177.5	174.5 174	165.5 164	163.5
30 31 32	8 8 8 4	32	37	3.9 0.4	4.4 1.2	43 44	4.5

RESULT 1 159355	synaptocagmin IV - rat C;Species: Rattus norvegicus (Norway rat)	C;Date: 02-Jul-1996 #Bequence_revision 02-Jul-1996 #text_change 13-Aug-1999 C;Accession: 159355; 158163	R;Vician, L.; Lim, I.K.; Ferguson, G.; Tocco, G.; Baudry, M.; Herschman, H.R. Proc. Natl. Acad. Sci. U.S.A. 92, 2164-2168. 1995	A; Title: Synaptotagmin IV is an immediate early gene induced by depolarization in PC12. A; Reference number: 159355; MUID: 95199319. PMTD: 2803344	A;Status: preliminary: translates for a formal and a form	A.Molecule type: mRNA	A;Residues: 1-425 <res></res>	A:Cross-references: GB:L38247; NID:g598376; PIDN:AAA67327.1; PID:G598377	Kiullich, B.; Ll, C.; Zhang, J.Z.; McMahon, H.; Anderson, R.G.; Geppert, M.; Sudhof, T Neuron 13, 1281-1291, 1994	A)Title: Functional properties of multiple synaptotaomins in brain.

A) Reference number: ISB163; MUID:95085772; PMID:7993622
A) Accession: ISB163; MUID:95085772; PMID:7993622
A) Accession: ISB163
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-425 < RE2>
A; Cross-references: EMBL:U14398; NID:9550453; PIDN:AAA68519.1; PID:9550454
C; Superfamily: synaptotagmin; protein kinase C C2 region homology
F; 147-262/Domain: protein kinase C C2 region homology < KC2B>
F; 281-396/Domain: protein kinase C C2 region homology < KC2B>

Gaps 0; Length 425; Indels 91.1%; Score 2006; DB 2; 89.9%; Pred. No. 5.9e-132; ive 21; Mismatches 22; Query Match
Best Local Similarity 89.9
Matches 382; Conservative

I sytv

1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLFAWICCORKSSKSNKTPPYKFVHVLKGV

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120 180 120 240 9 DIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNPPKTNLKPGSPSDLEN ATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNIKEARGL PAMDEQSWISDPYIKWIILPEKKHKVKTRVIRKTLDPAFDETFIFYGIPYTQIQELALHF 121 19 61 셤 ਨੇ 셤 qq à ð

240 300 PAMDEQSMISDPYIKMIILPEKKHKVKTRVLRKTLDPVFDETFTFYGVPYPHIQELSLHF TILSFDRESRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQST 181 a ð g

prote - bov

protein - rat

LOM -

hypothetical prote doc2 protein - hum hypothetical prote

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C;Accession: S33318
R;Bommert, K.; Charlton, M.P.; DeBello, W.M.; Chin, G;J.; Betz, H.; Augustine, G.J.
R;Bommert, K.; Charlton, M.P.; DeBello, W.M.; Chin, G;J.; Betz, H.; Augustine, G.J.
A;Title: Inhibition of neurotransmitter release by C2-domain peptides implicates synapt
A;Reference number: S33318; MUID:93247639; PMID:8097867
A;Accession: S33318
                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-474 <PER>
A;Cross-references: GB:M55048; GB:J05711; NID:g158526; PIDN:AAA28925.1; PID:g158527
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are
                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: duplication; membrane trafficking; phospholipid binding; synaptic vesicle;
F;1-107/Domain: intravesicular #status predicted <INT>
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: B3902 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Accession: B3902
R;Perin, M.S.; Johnston, P.A.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.
J. Biol. Chem. 266, 615-622, 1991
A;Fitle: Structural and functional conservation of synaptotagmin (p65) in Drosophila
A;Reference number: A39052; MUID:91093190; PMID:1840599
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C;Species: Loligo pealeii (longfin squid)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 AMNKTLVFAIFDFDRFSKHDQIGEVKVPLCTIDLAQ-TIEEWRDLV--SVEGEGGGEKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 FVHVLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 NIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%; Score 623.5; DB 1; 34.9%; Pred. No. 9.2e-36; ive 66; Mismatches 144;
                                                                                                                                                                                                                                                                                                                                  A;Cross-references: FlyBase:FBgn0004242
A;Map position: 23B
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Matches 152; Conservative
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A,Tille: Ca(2+)-dependent and -independent activities of neural and non-neural synaptota A,Reference number: S58399; MUID:95312080; PMID:7791877

A,Recession: S58400

A,Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                         C.Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 13-Aug-1999 C.Accession: S58400 R.Li, C.; Ullrich, B.; Zhang, J.Z.; Anderson, R.G.W.; Brose, N.; Suedhof, T.
                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 13-Aug-1999
                                                                                                                           DIPCESLEEISVEFLVLDSERGSRNEVIGRLVLGATAEGSGGGHWKEICDFPRRQIAKWH
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                           301 INTLIVVVIKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.5%; Score 627.5; DB 2; Length 403; 36.2%; Pred. No. 3.8e-36; tive 72; Mismatches 127; Indels 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:U20106; NID:g643655; PIDN:AAA87725.1;
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N,Alternate names: p65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 28.5
Best Local Similarity 36.2
Matches 153; Conservative
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MLCDG 425
                                                                                                                                                                                            VLCDG 425
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A; Residues: 1-403 <LIC>
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C2B domain of IP4BP/synaptotagmin
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R.Geppert, M.; Archer III, B.T.; Suedhof, T.C.
J. Biol. Chem. 266, 13548-13552, 1391
A.Title: Synaptotagmin II. A novel differentially distributed form of synaptotagmin. A.Reference number: A39454; MUID:91310620; PMID:1856191
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                                                                                                                                                                                                                                                                                                                                                                                            230 YDFDRFSKHDIIGEVKVPMNIVDLGQPIEEWRDLQGGE--KEEPEK---LGDICTSLRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENAT
                                                                                                                                           123 PKLFLEGEKESVSPESLKSSTSLTSEEKOEKLGTLFFSLEYNFERKAFVVNIKEARGLPA
                                                                                                                                                                                                                                                                                                                                                                243 LSFDRFSRDDIIGEVLIPLSGIEL----SEGKMLMNREIIKRNVRKSSGRGELLISLCYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 STTNTLTVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 VFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAK
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                                                                                                                                                                                              -----EEKEPENLGKLOFSLDYDFQANQLTVGVLQAAELPA
                                                                                                                                                                                                                                                      183 MDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTI
                                                                                                                                                                                                                                                                                    10 EFDEIP----TVVGIFSAFGLVFTVSLFA---WICCQRKSSKSNKTPPYKFVHVLKGVDI
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                                                                                      ----ETGLTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: synaptotagmin; protein kinase C C2 region homology C;Keywonds: membrane trafficking C;Keywonds: membrane trafficking F;136-249/Domain: protein kinase C C2 region homology <KC2A> F;267-382/Domain: protein kinase C C2 region homology <KC2B>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
                                                                                      - KNAMNMKDMKGGODDDDA--
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-KNAMNMKDMKGGODDDA
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Best Local Similarity 35.61
Matches 151; Conservative
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A, Residues: 377-422 <GEP>
A, Cross-references: GB:M64488
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A; Residues: 1-422 <FUK>
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A,Molecule type: mRNA
A,Residues: 1-422 <GGEP-
A,Molecule type: mRNA
A,Residues: 1-422 <GGEP-
A,GEP-
A,Cross-references: GB:W64488; NID:g207144; PIDN:AAA63502.1; PID:g207145
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are th
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Reywords: duplication; glycoprotein; membrane trafficking; phospholipid binding; synap
E;1-60/Domain: intravesicular #status predicted <INT>
F;61-87/Domain: transmembrane #status predicted <ITM>
F;61-87/Domain: protein #status predicted <ITM>
F;81-8-282/Region: phospholipid binding #status predicted
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2A>
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R;Geppert, M.; Archer III, B.T.; Suedhof, T.C.
Biol. Chem. 266, 13548-13552, 1991
A;Title: Synaptotagmin II. A novel differentially distributed form of synaptotagmin.
A;Reference number: A39454; MUID:91310620; PMID:1856191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----ESTKS-----EVKLGKLQYSMDYDFQKGELTVNVIQAADLPGMD-M 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 RFSRDDIIGEVLIPLSGIELSEGKMIMN-REIIK--RNVRKSSGRGELLISLCYQSTTNT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 LIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIP 363
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                                                                                                                                                                                                                                                                                                                              10 BFDEIPTVVGIFSAFGLVFTVSLFAWICCQ----RKSSKSNKTPPYKFVHVLKGVDIYPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                      67 INSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPGSPSDLENATPKLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 SMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFD
                           A;Molecule type: mRNĀ
A;Residues: 1-403 <BOM>
A;Cross-references: EMBL:X72386; NID:g311734; PIDN:CAA51079.1; PID:g311735
                                                                                                                                                                                                                                                                                                                                                                10 EFDEIP----TVVGIFSAFGLVFTVSLFA---WICCQRKSSKSNKTPPYKFVHVLKGVDI
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                                                                                                       C;Superfamily: synaptotagmin; protein kinase C C2 region homology F;121-235/Domain: protein kinase C C2 region homology <KC2A> F;255-370/Domain: protein kinase C C2 region homology <KC2B>
                                                                                                                                                                                                                          Length 403;
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                                                                                                                                                                                                                 28.2%; Score 621; DB 2; Length 40:
35.6%; Pred. No. 1.1e-35;
tive 71; Mismatches 131; Indels
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992
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Best Local Similarity 35.6*
Matches 151; Conservative
                                                                                                                                                                                                                                             Best Local Similarity 35.6%
Matches 149; Conservative
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Best Local Similarity
A;Status: preliminary
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υp	172 LD-MGGTSDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTF-KVPYQELGGKTLVMAI 229	C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-Aug-1999 C;Accession: JH0415
λŏ	243 LSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYO 298	R; Wendland, B.; Miller, K.G.; Schilling, J.; Scheller, R.H.
· 40	YDFDRFSKHDIIGEVKVPMNTVDLGQPIEEWRDLQGGEKEEPEKLGDICTSLRYV	A:Title: District a expression of the p65 gene family. A:Reference number: HA013: MITH-0127391: DMID: 0054189
ò	RISKKKTHVKKCTPNAVFNELF 3	A; Accession: JH0415
Db	PTAGKLTVCILEAKNLKKMDVGGLSDPYVKIHLMQNGKBLKKKKTTVKKKTLNPYENESF 34	A; Notecome Lype: Hunn A; Residues: 1-527 HB:M64277: NID:G213112: PIDN:AAA49229.1: PID:G213113 A:Cross-references: GB:M64277: NID:G213112: PIDN:AAA49229.1: PID:G213113
2		
7 원		C;Superramily: synaptotagmin; protein kinase C C2 region homology C;Reywords: glycoprotein; membrane protein; synaptic vesicle F:51-78/homain: hydronhohic / 470.
à		F;230-343/Domain: protein kinase C C2 region homology <kc2a>F;362-477/Domain: protein kinase C C2 region homology <kc2b></kc2b></kc2a>
Dp	405 WHST, 408	76, 14, 15, 16, 16, 16, 16, 16, 16, 16, 16, 16, 16
į		<pre>Lucif match Sinilarity 31.5%; Pred. No. 1.1e-33; Matches 156; Conservative 88; Mismatches 140; Indels 111; Gaps 19;</pre>
S58399		VFT-VSLF-AWICCQRKSSKSN
C:Speci	orway rat)	Db 46 TRHIETDISVSLLSVIVIFCGIVLLGVSLFVSWKLCWIPWRDKGLNPQRRDSQHHPH 102
C; Acces	Corsion in April 1990	Oy 52 KFVHVLKGVDIYPENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLN 102
Nature A, Title	activities of neural and non-ne	Db 103 QHLHHHHSHFTDLTVERVDCGPEMPERS-YLDLE 135
A, Refer	D:95312080; PMID:779187,7	Qy 103 GNFP
A; Moleci	A;Status: preliminary A;Molecule type: mRNA	Db 136 -SYPESGIKLSQTSPDIPVDTSSGSKENNIPNAHSQQQVSAPPPATRFNSLPRPIPQQLS 194
A, Resid	1 -LIC> 	ESVSPESLKSSTSLTSEEKQEKLGT
C; Super F; 224-3	forms and the state of the stat	Db 195 SPERGTQADEKVEQVTSIGQIKPELYKQRSIDTEAKKHQKVNCGRINFMLRYTYTTEQLV 254
F;356-4	71/Domain: protein kinase C C2 region homology <kc2b></kc2b>	QY . 172 VNIKEARGLPAMDEQSMTSDPXIKMTILPEKKHKUKTRVLRKTLDPAFDETFTFYGIPYT 231
Query Best L	Mat	Db 255 VXILKALDELPAKDANGF-SDPYVKIYLLPDRKKKRGTKVHRKTLNPIFNETFQF-NVPFN 312
Matches	s 127; Conservative 64; Mismatches 10	QY 232 QIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRG 289
δy	115 PSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNI 174	Db 313 ELQNRKLHFSVYDFDRFSRHDLIGGVVLDNLLEFSDFSEDTTIW-RDILEATSEKAD-LG 370
qa	SCGKINFSLRYDYESETL	QY 290 ELLISLCYQSTTNTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCT 349
ζ	175 KEARGLPAMDEQSMISDPYIKMTILPEKKHKVKTRVIRKTLDPAFDETFTFYGIPYTQIQ 234	Db 371 BINFSLCYLPTAGRLTITIIKATNLKAMDLTGFSDPYVKASLICDERRLKKRKTSIKKNT 430
Op	252 LKAFDLPAKDFCG-SSDPYVKIYLLPDRKCKLQTRVHRKTLNPTFDENFHF-PVPYEELA 309	DISVEFLVLDSERGSRNEVIGOLVLGAAA
λŏ	235 ELALHFILLSFDRFSRDDIGBVLIPLSGIELSEGKMIMNREIIKRNVRKSSGRGE 290	
Op	310 DRKLHLSVFDFDRFSRHDMIGEVILDNLFEASDLSRETSIWKDIQYATSESVDLGE 365	Qy 410 DYPRRQIAKWHVLCD 424
λō.		Db 491 ANPREPIEGMHQLIE 505
qq	366 IMFSLCYLPTAGRLTLTVIKCRNIKAMDITGYSDPYVKVSLLCDGRRLKKKKTTIKKNTL 425	ס הידואם מ
čo do	351 NAVENELFVEDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICD 410	A40001 3 A40011 3 A40101  - Caenorhabditis elegans
		Nymiceinate names: ric-z C,Species: Caenorhabditis elegans
کم ل <del>ر</del>	411 YPRRQIAKWHVLCD 424 411 YPRRQIAKWHVLCD 424 484 VDPVITATUHTINF 400	C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 24-Sep-1999 C;Accession: A40707; T16226
3		c, B.J.; Rand, J.B.
RESULT (JH0415 synaptog	RESULT 8 JH0415 Synaptogamin o-p65-C - electric ray (Discopyge ommata) N;Alternate names: synaptic vesicle protein o-p65-C	A;Incle: Symptic function is impaired but not eliminated in Caenorhabditis elegans mut A;Reference number: A40707; MUID:93313960; PMID:8391930 A;Accession: A40707 A;Getatus: preliminary A;Molecula fune: mona
		Ajvorectae Lype: High

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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-422 <PER>A;Cross-references: GB:M55047; GB:J05710; NID:g338657; FIDN:AAA60609.1; FID:g338658
C;Comment: Synaptotagmins are a major component of synaptic vesicle membranes and are the C;Genetics:
A;Gene: GDB:SYT1; SYT
A;Gene: GDB:SYT1; SYT
A;Gene: GDB:SYT1; SYT
C;Comment: Synaptotagmin; protein kinase C C2 region homology
C;Superfamily: synaptotagmin; protein kinase C C2 region homology
C;Reywords: dimp:, duplication; glycoprotein; membrane trafficking; phospholipid binding
C;Reywords: dimp:, duplication; glycoprotein; membrane trafficking; phospholipid binding
C;Reywords: dimp:, fapture predicted <INT>
F;54-80/Domain: transmembrane #status predicted <INM>
F;61-422/Domain:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synaptotagmin (p65) in Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 VVSFCGLALLVVSLFVFWKLC------WPCWKSKLVAPNVSTLPQSISSAPTEVFET 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 DLSREATVWKDIHCATTESMDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDPY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 RHNSFRRHLPROMNVSSVDFSMGTEPVLORGETRISIGRIKPELYKOK-SVDSEGNRKDD 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 VKICGKLNFALQYDYENELLVVKIIKALDLPAKOSTG-TSDPYVKIYLLPDRKKKKFQTRV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 LRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 HRKTLNPLFDELFQF-PVVYDQLSNRKLHFSIYDFDRFSRHDMIGEVILD----NLFEVS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    403 VKVSLMCEGRRIKKRKITITKKNTLNPVYNEAIIFDIPPENVDOVSLCIAVMDYDRVGENE 462
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C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Dacession: A39052
C;Accession: A39052
C;Accession: A39052
C;Accession: A. Johnston, P.A.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, U. Biol. Chem. 266, 615-622, 1991
A;Title: Structural and functional conservation of synaptotagmin (p65) in D: A;Reference number: A39052; MUID:91093190; PMID:1840599
                                                                                                                                                                                                                                                                                                                                                                         20 IFSAFGL-VFTVSLFA-WICCORKSSKSNKTPPYKFVHVLKGVDIYPENLNS--KKKFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 VKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OEKLIGTILFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 MIMNREIIKRNVR----KSSGRGELLISLCYOSTINTLIVVVILKARHLPKSDVSGLSDPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DLENATPKLFLEGEKES ----VSPESLKSSTSLTSE
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                                                                                                                                                                                                                         Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 422;
                                                                                                                                                                                             26.9%; Score 52.,
34.6%; Pred. No. 1.5e-33;
+ive 72; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;136-382/Region: phospholipid binding #status experimental F;136-249/Domain: protein kinase C C2 region homology kKC2A>F;267-382/Domain: protein kinase C C2 region homology kKC2B>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDKNEV-KNKPAVPKNSLHLDLEKRDLNGNFP---KTNLK-
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    F;56-77/Domain: transmembrane #status predicted <TMM>F;74-224/Domain: cytoplasmic #status predicted <CTY>F;224-338/Domain: protein kinase C C2 region homology F;357-472/Domain: protein kinase C C2 region homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 VIGOLVLGAAAEGTGGEHWKEICDYPRROIAKWHVL
                                                                                                                                                                                                         Query Match
Best Local Similarity 34.6%
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maptotagmin I - human
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A;Experimental source: strain Bristol N2; clone F31E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Date: 30-Sep-1993 #sequence_revision 29-May-1998 #text_change 13-Aug-1999
C;Accession: PG6300
C;Accession: PG6300
J.N.; Plumier, J.C.L.; Currie, R.W.; Robertson, H.A.
Proc. Natl. Acad. Sci. U.S.A. 94, 2638-2641, 1997
A;Title: A novel seizure-induced synaptotagmin gene identified by differential display.
A;Reference number: PC6300; MUID:97226006; PMID:9122248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TNLKPGSPSDLENAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 AMDEQSMISDPYIKWTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 GMD-MSGTSDPYVKLYLLPEKKKKVBTKVHRKTLNPVFNETFIF-KVAFNEITAKTLVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 IYDFDRFSKHDQIGQVLIPLGKIDL--GAVIEEWKDIAPPPDDKEAEKS--LGDICFSLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 PKLFLEGEKESVSPESLKSSTSLTSEEKQE-KLGTLFFSLEYNFERKAFVVNIKEARGLP
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                                             A; Cross-references: GB:L15302; NID:g289717; PIDN:AAA28145.1; PID:g289718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Map position: 2
A;Introns: 39/2; 72/1; 132/3; 289/3; 329/1; 373/3; 408/2
A;Introns: 39/2; 72/1; 132/3; 289/3; 329/1; 373/3; 408/2
C;Superfamily: synaptotagmin; protein kinase C C2 region homology C;Keywords: membrane trafficking; transmembrane protein
E;153-266/Domain: protein kinase C C2 region homology «KC2A»
F;286-401/Domain: protein kinase C C2 region homology «KC2B»
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5;Superfamily: synaptotagmin; protein kinase C C2 region homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%; Score 594; DB 2; Length 441; 40.2%; Pred. No. 9.3e-34; tive 57; Mismatches 111; Indels
                                                                     R,Du, Z.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F31E8.
A;Reference number: Z18481
A;Accession: T16226
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 KKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 148; Conserv
A; Residues: 1-441 < NON>
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A, Residues: 1-498 <SAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: snt-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 LFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: synaptic vesicle protein o-p65-A
C;Species: Discopyge ommata
C;Date: 15-Jan-1993 #sequence revision 15-Jan-1993 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Rattus norvegicus (Norway rat)
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Aug-1997
                                                             263 LOSAR--KEEGEK---LGDICFSLRYVPTAGKLTVVILEAKNLKKOMDVGGLSDPYVKIHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 LQFSLDYDFQNNQLIVGIIQAAELPALDVGG-TSDPYVKVFVLPDKKKKYETKVHRKTIN
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                              272 LMNREIIKRNVRKSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPYVKVNL
                                                                                                                                                 332 YHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 KKNYKKGKEKGGKNAMTMKDVKEMGKSGKEQALKDEDEDAETGLTTDGKEEEKEDEKLGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Residues: 1-427 (WEN)
A:Residues: 1-427 (WEN)
A:Cross-references: GB:M64275; NID:g213108; PIDN:AAA49227.1; PID:g213109
A:Cross-references: GB:M64275; NID:g213108; PIDN:AAA49227.1; PID:g213109
A:Cross-references: GB:M64275; NID:g213108; PIDN:AAA49227.1; PID:g213109
A:Cross-references: GB:M64275; NID:g213108; PIDN:AAA49227.1; PID:g213109
A:Cross-references: GB:M64275; NID:g213108; CC region homology
C;Reywords: GIV:Momain: hydrophobic (HYD)
F:141-254/Domain: protein kinase CC cregion homology (KC2A)
F:26/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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26.3%; Score 579.5; DB 2; Length 427;
Best Local Similarity 38.8%; Pred. No. 9.1e-33;
Matches 128; Conservative 66; Mismatches 115; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 KTNLKPGSPSDLENA----TPKLFLEGEKESVSPESLKSSTSLTS--
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R;Perin, M.S.; Fried, V.A.; Mignery, G.A.; Jahn, R.; Suedhof,
Nature 345, 260-263, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: JH0413
R; Wendland, B; Miller, K.G.; Schilling, J.; Scheller, R.H.
Neuron 6, 993-1007, 1991
A; Title: Differential expression of the p65 gene family.
A; Reference number: JH0413; WUID:91273991; PMID:2054189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synaptotagmin o-p65-A - electric ray (Discopyge ommata)
                                                                                                                                                                                                                                                                                                           393 LGAAAEGTGGEHWKEICDYPRRQIAKWHVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synaptotagmin P65 - rat
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NyAlternate names: 39K protein; synaptic vesicle protein p65
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Sep-1933 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C;Accession: A45486, S12272
R;Davletov, B.; Sontag, J.M.; Hata, Y.; Petrenko, A.G.; Fykse, E.M.; Jahn, R.; Sudhof, A.Biol. Chem. 268, 6816-6822, 1993
A;Title: Phosphorylation of synaptotagmin I by casein kinase II.
A;Reference number: A45486, MUID:93203288; PMID:8454654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:128028, NCBIP:128029)
R;Tugal, H.B., van Leeuwen, F.; Apps, D.K.; Haywood, J.; Phillips, J.H.
Biochem. J. 279, 699-703, 1991
A;Title: Glycosylation and transmembrane topography of bovine chromaffin granule p65.
A;Reference number: S19272; MUID:92061982; PMID:1719959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 MQNGKRLKKKKTIIKKNTINPYYNESFSFEVPFEQIQKVQVVYTVLDXDKIGKNDAIGKV 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 FKKKNKKKGKEKGKKNAINMKDVKDLGKTMKDQALKDDDAETGLTDGEEKEEPKEEEKLG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIEL----SEGKM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQL 391
                                                                                                                                                             FKKKNKKKGGEKGEKGGKNAINMKDVKDLGKTMKDQALKDDDAETGLTDGEEKEEPKEEEKLG
                                                                                                                                                                                                                                                                   204 NPVFNEQFTF-KVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEEWRD
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A;Cross-references: GB:L05922; NID:g945210; PIDN:AAA87360.1; PID:g945211
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C;Superfamily: synaptotagmin; protein kinase C C2 region homology
F;136-249/Domain: protein kinase C C2 region homology <KC2A>
F;267-382/Domain: protein kinase C C2 region homology <KC2B>
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                        Pred. No. 7e-33;
; Mismatches 114; Indels
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                                                       Conservative
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                        Local Similarity
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A,Rolecule type: 145-168;201-212;214-216;237-244;333-354;357-366;376-388;392-398 <PER2>
A,Note: 99-Asp, 116-Glu, 169-Arg, and 232-Glu were also found
C,Superfamily: synaptotagmin; protein kinase C Cz region homology
C,Keywords: calmodulin binding; glycoprotein; membrane trafficking; synaptic vesicle; tr
F;152-709Domain: intravesicular #status predicted <INT>
F;53-79Domain: extravesicular #status predicted <INT>
F;80-421/Domain: extravesicular #status predicted <EXT>
F;135-248JOmmain: protein kinase C Cz region homology <KC2A>
F;266-381/Domain: protein kinase C Cz region homology <KC2B>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
A;Title: Phospholipid binding by a synaptic vesicle protein homologous to the regulatory A;Reference number: S09595; MUID:90238548; PMID:2333096
A;Accession: S09595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 LMNREIIKRNVRKSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPYVKVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 577; DB 2; Length 421; Pred. No. 1.3e-32; 64; Mismatches 115; Indels
                                                                                A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%;
39.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 26.2%
Best Local Similarity 39.9%
Matches 132; Conservative
                                                                                                   A, Molecule type: mRNA
A, Residues: 1-421 <PER1>
A, Accession: S20211
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R,Lou, X.; Bixby, J.L.
Dev. Biol. 159, 327-337, 1993
A;Title: Coordinate and noncoordinate regulation of synaptic vesicle protein A;Reference number: 151210; MUID:93374184; PMID:8365570

A;Cross-references: GB:S64957; NID:g409527; PIDN:AAB28081.1; PID:g409528

A;Accession: 151210 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA

A; Residues: 1-424 <LOU>

C;Superfamily: synaptotagmin; protein kinase C C2 region homology F;138-251/Domain: protein kinase C C2 region homology <KC2> F;269-384/Domain: protein kinase C C2 region homology <KC2B>

synaptotagmin p65 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 13-Aug-1999
C;Accession: 151210

11;

Gaps

26.1%; Score 575; DB 2; Length 424; 37.0%; Pred. No. 1.8e-32; Live 71; Mismatches 129; Indels 40;

Query Match
Best Local Similarity 37.0%;
Matches 141; Conservative

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68 NSKKKFGADDKNEVKNKPAVPKNSLHLD-----

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                                                       115 PSDLENATPKLFLEGEKESVSPESLK---SSTSLT-SEEKQ-----EKLGTLFFSLEYNF
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ORGANISM: Homo sapiens
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Sequence 1072, App
Sequence 1072, Ap
Sequence 368, App
Sequence 365, App
Sequence 365, App
Sequence 365, App
Sequence 81, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 81, Appl
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6, Appli
                                                  February 20, 2004, 13:12:55; Search time 40 Seconds (without alignments) 2224.687 Million cell updates/sec
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version 5.1.6
- 2004 Compugen Ltd.
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US-09-764-875-772

US-09-764-870-368

US-09-764-870-368

US-10-125-540-365

US-10-125-540-365

US-10-125-540-365

US-10-231-913-81

US-10-231-913-81

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US-10-231-913-81

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US-10-231-913-81

US-10-231-913-81
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                                                                                                                                                801455 seqs, 209382283 residues
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Maximum Match 100%
Listing first 45 summaries
                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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seq length: 200000000
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19	447	0	413	11	US-09-978-418-24	equence 24,
20	418	6	412	77	US-09-764-875-683	683
21	395.5	8	373	12	875-77	Sequence 770, App
22	395.5		375	12	US-09-764-875-898	8
23	344	'n	199	12	US-09-764-875-771	773
24	330	Ŋ.	234	12	US-09-764-875-767	76
25	330		267	σ	US-09-764-870-359	359,
26	330	15.0	267	15	US-10-125-540-359	Sequence 359, App
27	321.5	•	671	12	US-10-311-626-5	5, App
28	320.5		671	12	4	2460,
29	319.5		219	10	US-09-925-300-1448	1448,
30	301.5		555	12	m	e 2530,
31	296.5	•	208	σ	US-09-764-870-497	97, A <u>I</u>
32	296.5		208	12	US-09-764-875-1071	10
33	296.5	•	208	15	US-10-125-540-497	49
34	254.5	•	501	15	US-10-177-293-447	Sequence 447, App
35	253	•	407	σ	US-09-764-870-375	Sequence 375, App
36	253	٠	407	15	3-10-125-540-37	s 375
37	250	٠	862	77	US-10-339-782-492	492
38	250	11.4	910		-10-177-293-44	449
39	245		376	15	-10-177-293-45	451,
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41	235.5	10.7	336	12	7	22,
42	235.5		348	9	-764-870-5	ш
43	235.5	10.7	348	12	3-09-764-	
44	235.5	0	348	15	-10-125-540-50	502
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	AL INFOR	MATION:				
	APPI,ICANT: French.	rench.	Cynthia K	×		

APPLICANT: French, Cynthia K.
APPLICANT: Yamanoto, Karen K.
TITLE OF INVENTION: Method for Identifying Hormonally Modulated Genes FILE REFERENCE: 267/116
CURRENT APPLICATION NUMBER: US/09/954,570
CURRENT FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1

1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVSLFAWICCQRKSSKSNKTPPYKFVHVLKGV Gaps · 0 425; Length Indels 100.0%; Score 2201; DB 11; 100.0%; Pred. No. 1.3e-195; ative 0; Mismatches 0; Matches 425; Conservative Similarity

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1 MABITNIRPSFDVSPVVAGLIGASVLVVCVSVTVFVWSCCHQQAEKKHKNPPYKFIHMLK 60
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US-09-764-875-772
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MARREN. Bridget A.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: TEB. Sally,
TITLE OF INVENTION: SECRETION AND TRAFFICKING MOLECULES
FILE REFERENCE: PF-0801 PCT
CURRENT APPLICATION NUMBER: US/10/311, 626
CURRENT FILING DATE: 2002-12-17
PRIOR APPLICATION NUMBER: 60/215,465; 60/239,384; 60/253,639
PRIOR FILING DATE: 2000-06-29; 2000-10-10; 2000-11-28
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Incyte ID No. US20030186379A1 7946329CD1
US-10-311-626-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRIBOULEY, Catherine M.
LU, Dyung Aina M.
HAFALIA, April
                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/10311626 Publication No. US20030186379A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti
APPLICANT: TANG, Y. Tom
APPLICANT: YIE, Henry
APPLICANT: CHAMLA, Narinder K.
APPLICANT: BAUGHN, Mariah R.
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YAO Monique G.
GURURAJAN, Rajagopal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           John D.
Gregory A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BANDMAN, Olga
ELLIOT, Vicki S.
NGUYEN, Danniel B.
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LEE, Ernestine A.
XU, Yuming
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| : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | : :||| | :
59 GVDIYPENINSKKKF-----GADDKNEVKNKPAVPKNSLHIDIEKRDINGNFPKTNIKPG 113
                                                                                                                                                                                                                                               114 SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKA 169
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                                                                                 FVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIP
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Publication No. US20040018969A1
GENERAL INFORMATION:
APPLICANT: ROBER et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ02
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249
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US-10-231-913-12
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                                              270 KMLMNREIIKRNVR----KSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDP 325
                                                                                                                                                                                                              326 YVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRN 385
                                                                                                                                                                                                                                            402 YVXVSLMCEGRRLKKRKTTTXXATLNPVYNEALIFDIPPENVDQVSLSIAVMDYDRVGHN 461
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                      210 VLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEG 269
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                                                                                                                                                             342 SDLSREATVWKDIHCATTESIDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDP
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                         462 EVIGUCRIGLDAEGLGRDHWNEMLAYHRKPITHWHPLLE 500
                                                                                                                                                                                                                                                                                                                 386 EVIGOLVLGAAAEGTGGEHWKEICDYPRROIAKWHVLCD 424
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OTHER INFORMATION: Xaa equals any of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 368, Application US/09764870 Patent No. US20020042386A1
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OTHER INFORMATION: Xaa
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
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US-09-764-875-1072
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LENGTH: 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-216
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CURRENT FILING DATE: 2002-08-30
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PRIOR APPLICATION NUMBER: 60/251,660
PRIOR PILING DATE: 2000-12-08
PRIOR PILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 2001-01-08
PRIOR PILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR PILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-07
PRIOR PILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-24
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PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-09-12
Application US/10231913
No. US20040005576A1
                                                                                                                                                                                                                                                             Spytek, Kimberly A. Shenoy, Suresh G. Alsobrook II, John P. Edinger, Schlomit Peyman, John A. Stone, David J. Ellerman, Karen Gangolli, Esha A.
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Spaderna, Steven K.
Zerhusen, Bryan D.
                                                                                                                                                                                        Malyankar, Uriel M.
Tchernev, Velizar T.
Vernet, Corine A.
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Casman, Stacie J.
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Colman, Steven D.
Eisen, Andrew J.
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Matches 159; Conservative
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SOFTWARE: Patentin Ver. 2.1
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                                                                       Guo, Xiaojia S.
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-09-764-875-1072
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                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZO2
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 188;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti
FILE REPERENCE: PTZIACI
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
Sequence 1072, Application US/09764875
Publication No. US20040018969A1
GENERAL INFORMATION:
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Best Local Similarity 58.4%
Matches 108; Conservative
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LENGTH: 188
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LENGTH: 188
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LOCATION: (2) - OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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152 PTSIGRIKPELY---KQKSVDGEDAKS-----EATKSCGKINFSLRYDYETETLIVRI
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                                                                              NAME/KEY: misc_feature
LOCATION: (10)_
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-10-125-540-368
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Batent No. US20020042386A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PIZI4

CURRENT APPLICANT UNUBER: US/99/764,870

CURRENT FILING DATE: 2001-01-17
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252 LKAFDLPAKDFCG-SSDPYVKIYLLPDRKCKIQTRVHRKTLNPTFDENFHF-PVPYBELA 309
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TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFRENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
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PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR PELING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-12
PRIOR PELING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
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PRIOR PELING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-24
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-04-24
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PRIOR FILING DATE: 2001-08-20
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PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                     Liu, Xiaohong
Padigaru, Muralidhara
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                      Peyman, John A.
Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
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486 YPRKPIAHWHCLAE
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351 NAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICD 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 461;
                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.4%; Score 603; DB 15; Length 4
40.8%; Pred. No. 3.7e-47;
tive 62; Mismatches 104; Indels
                                                                                                                                                                                                                  US-10-125-540-365

Sequence 365, Application US/10125540
; Publication No. US20030059875A1
; GENERAL INFORMATION:
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Publication No. US20040005576A1
GENERAL INFORMATION:
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Alsobrook II, John P.
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Tchernev, Velizar T.
Vernet, Corine A.
Spytek, Kimberly A.
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Shimkets, Richard A.
Casman, Stacie J.
                                                                                                                          436 YPRKPIAHWHSLVE 449
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436 YPRKPIAHWHSLVE 449
                                                                                 411 YPRRQIAKWHVLCD 424
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APPLICANT: Li, Li
APPLICANT: Patturajan, Me
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ORGANISM: Homo sapiens
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60 VVSFCGLALLVVSLEVFWKLC------WPCWKSKLVAPNVSTLPQSISSAPTEVFET 110
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APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.9%; Score 592; DB 12; Length 49
Best Local Similarity 34.6%; Pred. No. 4.4e-46;
Matches 158; Conservative 72; Mismatches 156; Indels
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CURRENT APPLICATION NUMBER: US/10/231,913

CURRENT FILING DATE: 2002-08-30

PRIOR APPLICATION NUMBER: 60/251,660

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2001-012-12

PRIOR FILING DATE: 2001-012-08

PRIOR FILING DATE: 2001-012-08

PRIOR FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 60/269,942

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR FILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/286,183

PRIOR APPLICATION NUMBER: 60/286, 183

PRIOR APPLICATION NUMBER: 60/313,627

PRIOR APPLICATION NUMBER: 60/313,627

PRIOR FILING DATE: 2001-08-20

PRIOR FILING DATE: 2001-08-20

PRIOR FILING DATE: 2001-09-12

NUMBER OF SEQ ID NOS: 292

NUMBER OF SEQ ID NOS: 292
                                                                                                                                                                                                                                                      Sequence 80, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
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Tchernev, Velizar T.
Vernet, Corline A.
Spytek, Kimberly A.
Shenoy, Suresh G.
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Edinger, Schlomit
Peyman, John A.
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APPLICANT: Li, Li
Batturajan, Mera
APPLICANT: Binketes, Richard A.
APPLICANT: Casman, Stacie J.
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Bllerman, Karen
Gangolli, Esha A.
Boldog, Ference L.
Colman, Steven D.
                                                                                                                486 YPRKPIAHWHSLVE 499
                                                                           411 YPRRQIAKWHVLCD 424
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Liu, Xiaohong
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US-10-231-913-80
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 ILISLCYQSTINTLTVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTP 350
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27.2%; Score 598; DB 12; Length 511;
Best Local Similarity 40.4%; Pred. No. 1.3e-46;
Matches 127; Conservative 63; Mismatches 104; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Spaderna, Steven K.
APPLICANT: Zerbusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR PELICATION NUMBER: 60/251,660
PRIOR PELICATION NUMBER: 60/260,326
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-02-20
PRIOR FILING DATE: 2001-04-24
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR PLING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR PRIOR DATE: 2001-04-20
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Colman, Steven D.
Eisen, Andrew J.
Liu, Kiaohong
Padigaru, Muralidhara
                                                                                                                Casman, Stadie J.

Malyankar, Uriel M.
Tchernev, Velizar T.
Vernet, Corine A.
Spytek, Kimberly A.
Spytek, Kimberly A.
Spytek, Suresh G.
Alsobrook II, John P.
Edinger, Schlomit
Peyman, John A.
Stone, David J.
Ellerman, Karen
Gangolli, Esha A.
                                                                      Patturajan, Meera
Shimkets, Richard A.
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NUMBER OF SEQ ID NOS: 292
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
LENGTH: 511
                    Guo, Xiaojia S.
Li, Li
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; ORGANISM: Mus musculus
US-10-231-913-81
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APPLICANT:
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PRIOR FILING DATE: 2001-08-20
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Best Local Similarity
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151 QEKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRV 210
                                                                                                                                                 229 VKICGKLNFALQYDYENELLVVKIIKALDLPAKDSTG-TSDPYVKIYLLPDRKKKRQTRV 287
                                                                                                                                                                                                                                  288 HRKTLNPLFDELFQF-PVVYDQLSNRKLHFSIYDFDRFSRHDMIGEVILD----NLFEVS 342
                                                                                                                                                                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                     403 VKVSLMCEGRRLKKRKTTTKKNTLNPVYNEAIIFDIPPENVDQVSLCIAVMDYDRVGHNE 462
                                                       --DLENATPKLFLEGEKES----VSPESLKSSTSLTSE----EK 150
                                                                                          170 RHNSFRRHLPRQMNVSSVDFSMGTEPVLQRGETRTSIGRIKPELYKQK-SVDSEGNRKDD 228
                                                                                                                                                                                                   211 LRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGK 270
                                                                                                                                                                                                                                                                                               343 DLSREATVWKDIHCATTESMDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDPY 402
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                                                                                                                                                                                                                                                                       271 MIMNREIIKRNVR----KSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPY
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IIILE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
                                                                                                                                                                                                                                                                                                                                                                                                                                             387 VIGOLVLGAAAEGTGGEHWKEICDYPRRQIAKWHVL 422
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CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/269,942
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Publication No. US20040005576A1
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Tchernev, Velizar T.
Verner, Corine A.
Spytek, Kimberly A.
Shenoy, Sureah G.
Alsobrook II. John P.
Bdinger, Schlomit
Peyman, John A.
Stone, David J.
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Padigaru, Muralidhara
Spaderna, Steven K.
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Boldog, Ference L.
Colman, Steven D.
Eisen, Andrew J.
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Gangolli, Esha A.
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Li, Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 LSREATVWKDIHCATTESIDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDPYV 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 HNSFRRHLPROMNVSSVDFSVGTEPILQRGETRISIGRIKPELYKQK-SVDSEGNRKDDV 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 DDKNEVKN------KPAVPKNSLHLDL-----EKRDLNGNFPKTNLKPGSPS-
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                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                        Length 523;
                                                                                                                                                                                                                                                                                     Query Match 26.8%; Score 590; DB 12; Length 52:
Best Local Similarity 33.7%; Pred. No. 7.3e-46;
Matches 154; Conservative 74; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 IGQLVLGAAAEGTGGEHWKEICDYPRRQIAKWHVLCD 424
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PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 79
LENGTH: 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 78, Application US/10231913; Publication No. US20040005576A1; GENERAL INFORMATION:
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APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsobrook II, John P.
APPLICANT: Alsobrook II, John P.
APPLICANT: Binger, Schlomit
APPLICANT: Binger, Schlomit
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Gangolli, Esha A.
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Eisen, Andrew J.
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                                                                                                                                                                          TYPE: PRT ORGANISM: Mus musculus
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Job time : 41 secs
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerbusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 589; DB 12; Length 5; Pred. No. 9.1e-46; 73; Mismatches 157; Indels
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                                                                                                                                   THIE REFERENCE: 21402-216

CURRENT APPLICATION NUMBER: US/10/231,913

CURRENT APPLICATION NUMBER: US/10/231,913

CURRENT APPLICATION NUMBER: 60/251,660

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-12

PRIOR FILING DATE: 2001-01-08

PRIOR FILING DATE: 2001-01-08

PRIOR APPLICATION NUMBER: 60/263,800

PRIOR APPLICATION NUMBER: 60/263,800

PRIOR PILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/264,942

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-01-24

PRIOR APPLICATION NUMBER: 60/266,183

PRIOR APPLICATION NUMBER: 60/266,183

PRIOR APPLICATION NUMBER: 60/313,627

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: 60/313,627

PRIOR PILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: 60/318,712

PRIOR APPLICATION NUMBER: 60/318,712

PRIOR APPLICATION NUMBER: 60/318,712

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

PRIOR APPLICATION NUMBER: 60/318,712

PRIOR PILING DATE: 2001-08-20

PRIOR PILING DATE: 2001-08-20

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PRIOR PILING DATE: 201-08-20

PRIOR PILING DATE: 2001-08-20

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US-10-231-913-78
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; Sequence 6, Application US/10307389; Publication No. US20030175807A1; GENERAL INFORMATION:

US-10-307-389-6

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APPLICANT: LE MOUBLIC, HERVE
APPLICANT: LE MOUBLIC, HERVE
APPLICANT: BRULET, FILIPPE
TITLE OF INVENTION: CHIMBRIC CELL LEVEL
TITLE OF INVENTION: AT THE SINGLE CELL LEVEL
FILE REPERENCE: 03495-0207-00000
CURRENT APPLICATION NUMBER: US/09/863,901
FILE REPERENCE: 2002-12-02
FRIOR APPLICATION NUMBER: US/09/863,901
PRIOR PLILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR PLILING DATE: 2000-06-01
PRIOR PLILING DATE: 2000-06-06
PRIOR PLILING DATE: 2000-06-06
PRIOR PLILING DATE: 2000-06-06
PRIOR PLILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 NPVFNEQFTF-KVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEEWRD 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 FPKTNLKPGSPSDLENATPKLFLEGEKESVSPESLK---SSTSLT-SEEK----QEKLG
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Best Local Similarity 39.9%;
Matches 132; Conservative 6
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US-10-307-389-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schneider, Cynthia K.
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneider, Patrick A.
APPLICANT: Yamamoto, Karen K.
TITLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,246
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRARION NUMBER: 32,944
REGISTERATION NUMBER: 32,944
US-08-609-049A-12
US-09-170-996-12
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US-09-170-996-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-036-315-2
; Sequence 2, Application US/09036315
; Patent No. 6218523
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TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 425 amino acids
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                                               MOLECULE TYPE: protein
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Matches 425;
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ZIP: 9411
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                        GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-036-315-5

US-09-036-315-10

US-08-036-315-10

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US-08-036-315-24

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US-09-049A-13

US-09-049A-18

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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
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Maximum DB seq length: 200000000
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2201
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Match Length
                                                 Copyright
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Perfect score:
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
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Patent No. 6218523
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COMPUTER: IBM PC compatible
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LENGTH: 425 amino acids
TYPE: amino acid
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Best Local Similarity 89.9*
Matches 382; Conservative
INFORMATION FOR SEQ ID NO:
                                              TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                         ; LOCATION: 1..425
; OTHER INFORMATION:
US-09-036-315-5
                                                                                                                                          NAME/KEY: Protein
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421 MLCDG 425
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US-09-036-315-7
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APPLICANT: French, Cynthia K.
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneider, Raren K.
APPLICANT: Pramamoto, Karen K.
TITLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOTTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315 FILING DATE: 06-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 018002-000210US TELECOMMUNICATION INFORMATION:
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COUNTRY: USA
ZIP: 94111-3894
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WENTER: IBM PC compatible
"WENTER: IBM PC compatible
"WENTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PATOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,246
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US-09-036-315-5
; Sequence 5, Application US/09036315
; Patent No. 6218523
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(415) 576-0300
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STATE: California
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APPLICANT: French, Cynthia K.
APPLICANT: Schneider, Patrick A.
APPLICANT: Schneider, Naren K.
TITLE O'NTWENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
/note= "rat synaptotagmin 4
                                                                                    91.1%; Score 2006; DB 3;
89.9%; Pred. No. 8.9e-197;
iive 21; Mismatches 22;
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204 NPVFNEQFTF-KVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNIVDFGHVTEEWRD 262
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; Patent No. 6216523
; GENERAL INFORMATION;
APPLICANT: French, Cynthia K.
APPLICANT: Schneider, Patrick A.
; APPLICANT: Yamamoro, Kazen K.
; TITLE OF INVENTION: Prostate Cancer-Specific Marker NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew Librer STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.4%; Score 581; DB 3; 39.9%; Pred. No. 7.5e-51;
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                                                                                                                                                PF-0320 US
                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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STATE: California
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94111-3834
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          018002-000210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Incyte Pharmaceuticals, Inc
                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PRIOR APPLICATION NUMBER: US 60/041,246
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-0002
TELECOMMUNICATION INFORMATION:
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FILING DATE: Herewith
      US/09/036,315
                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acide
STRANDEDNESS:
TOPDIACY
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Patent No. 6074844
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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      APPLICATION NUMBER: US/09
FILING DATE: 06-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Peptide
LOCATION: 1..121
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 A 396
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215

Gaps

20;

Length 422; Indels

us-09-680-121c-2.rai

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OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0320 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
CAMPUTTER: IBM Compatible
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 355 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 30.23
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 PRRQIAKWHVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 ARRPIAQWHHL 332
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CONDERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                     STRANGE ILLEGATION TOPOLOGY: LILEGATE SOURCE:
LIBRARY: GenBan
                                                                                                                                                                                                                                                                                                                                                GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KOEKLGTLFFSLEYNFERKAFVVNIKEARGLPAMDEOSMISDPYIKMILLPEKKHKVKTR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 VLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLS 262
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: ALILMEN, Preeti
APPLICANT: Lal. Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%; Score 577; DB 3; Length 113;
100.0%; Pred. No. 2.3e-51;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Repro-PC-1.0 (PC-20) internal repeat (amino acid positions 150-263)"
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
                                                                                        CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
FILING DATE: 15-MAY-1997
FILING DATE: 07-MAR-1997
ATTORNEY AGENT INFORMATION:
NAME: SLOCELLA, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMBUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FSELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,979
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08872979
Patent No. 6074844
                                                                                                                                                                                                                                                                                                                                                                                                                  : 113 amino acids
amino acid
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Best Local Similarity 100.
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1.113
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Peptide
LOCATION: 1..113
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                                                                                    CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-036-315-10
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130 EKESVSPESLKSSTSLTSEEK------QEKLGTLFFSLEYNFERKAFVVNIKEAR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 AVENELEVFDIPCEGLEDISVEFLVLDSERGSRNEVIGGLVLGAAAEGTGGEHWKEICDY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 PYFNEAFVFLVPVSQLQSVDLVLAVWARGLQLRTEPVGKVLLGSRASGQPLQHWADMLAH 321
                                                                                                                                                                                                                                          179 GLPAMDEQSMISDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELAL 238
                                                                                                                                                                                                                                                                                                                                                            239 HFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKR------NVRKSSGRGEL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 LISLCYQSTINTLIVVVILKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPN 351
                                                                                                                                                       39 DKETVGLGSARNSTITHLVQPDVDCLEPCSGGDQQWGRLLLSLEYDFGSQEIRVGLRQAG 98
16.4%; Score 361.5; DB 3; Length 355; 30.2%; Pred. No. 1.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08872979
Patent No. 6074844
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Pereti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inforte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                          Mismatches 120;
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199 LPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides NUMBER OF SEQUENCES: 32
CORRESSPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 60;
      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,049A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.1%; Score 310; DB 3; I 100.0%; Pred. No. 1.8e-24;
                                                                                                       FILING DATE: 0.00-MRR.1998
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,246
FILING DATE: 0.7-MAR-1997
ATTORNEY/AGRY INFORMATION:
NAME: SEOTELLA JOHN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
TELEPAX: (415) 576-0300
SEQUENCE CHARACTERISTICS:
TENEMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION 1435
FILING DATE: 29-FEB-1>>
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-063700US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08609049A Patent No. 5948664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100. Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide
US-09-036-315-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-08-609-049A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TSEEKQEKLGILFFSLEYNFERKAFVVNIKEAR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 DL----MPGGTVDPYARVSVSTQAGHRHETKVHRGTLCPVFDETCCFH-IPQAELPGAIL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 HFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKR-----NVRKSSGRGEL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 LISLCYQSTINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTPN 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 AVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGGLVLGAAAEGTGGEHWKEICDY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 35;
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Patent No. 6218523
GENERAL INFORMATION
APPLICANT: Schneider, Patrick A.
APPLICANT: Yamamoto, Karen K.
TILLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%; Score 338.5; DB 3; 29.8%; Pred. No. 4.2e-26; tive 61; Mismatches 118;
                                                                                                                                                                                                             PF-0320 US
    US/08/872,979
                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36, 749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 EKESVSPESLKSSTSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.8
Matches 91; Conservative
APPLICATION NUMBER: UN FILING DATE: Herewith
                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                         FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: LUNGNOT12
CLONE: 1003941
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-09-036-315-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-08-872-979-3
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289 GELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKC 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.120
CTHER INFORMATION:
CTHER INFORMATION:
US-09-036-315-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
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                                                                                                                                                                                                                                                                                                                           72 TLNPYFNESFSFEIPFEQIQKVQVVVTVLDYDKLGKNEAIGKIFVGSNATGTELRHWSDM 131
                                                                                                                                                                                                                                           Gaps
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APPLICANT: Williams, Lewis T.
APPLICANT: Wolz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220el PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 288; DB 3; Length 138; 46.8%; Pred. No. 1.3e-21; Live 22; Mismatches 45; Indels
                                                                                                                                      13.1%; Score 288; DB 2; Length 138; 46.8%; Pred. No. 1.3e-21; tive 22; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,049
FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09170996 Patent No. 6291220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 amino acids
      LENGTH: 138 amino acids
                                                                                                                                                                                59; Conservative
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                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  409 CDYPRR 414
                                                                                                                                                                                                                                                                                                                                                                                                                      132 LANPRR 137
                                                                                                                                                          Best Local Similarity
Matches 59; Conserv
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                                                                                                 US-08-609-049A-17
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US-09-170-996-17
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                                                                                                                                          Query Match
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59; Conservative

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S KEEEKLGKLQYSLDYDFQNNQLLVGIIQAAELPALD-MGGTSDPYVKVFLLPDKKKKFFT
                                                                       349 TPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09036315
Patent No. 6218523
GENERAL INFORMATION:
APPLICANT: French, Cynthia K.
APPLICANT: Yamamoto, Karen K.
TITLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING STSTEM: TECLOLOFMS-LOOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
CLASSIFICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,246
FILING DATE: 15-MAY-1997
PRIOR APPLICATION NUMBER: US 60/041,246
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: STOOTHIA, OADN R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELECOMMUNICATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELECOMMUNICATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 018002-000210US
TELEPHANE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Townsend and Townsend an STREET: Two Embarcadero Center, Eight CITY: San Francisco STATE: California COUNTRY: USP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 45.3%
Matches 53; Conservative
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Sequence 25, Application US/09036315
Patent No. 6218523
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                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-609-049A-16
US-09-036-315-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 KVHRKTLNPVFNEQFTF-KVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVD 119
                 209 RVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIE 265
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repeat (amino acid positions 268-383)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.1%; Score 244; DB 3; Length 115; 45.3%; Pred. No. 3e-17; ive 23; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 TPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLG 394
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Patent No. 6218523
GENERAL INFORMATION:
APPLICANT: Schneider, Patrick A.
APPLICANT: Yamanoto, Karen K.
TITLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSERE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWALLY SIDER:
SOFTWALE STILER:
SOFTWALE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998
CLASSIFICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997
FILING DATE: 15-MAY-1997
FILING DATE: 07-MAR-1997
FILING DATE: 07-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REFERENCE/DOCKET NUMBER: 018002-000210US
TELEFONMUNICATION INFORMATION:
TELEFONDE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 115 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1.115
OTHER INFORMATION:
OTHER INFORMATION:
JS-09-036-315-8
                                                                                                                                                                                                                                                                                                                                                                                                                   California
: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 48; Conserv:
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                                                                                                                     RESULT 12
US-09-036-315-8
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STATE:

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Gaps
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Patent No. 5948664
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 5948664el PI 3-Kinase Polypeptides
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 IPLSGIELSEGKWLMNREIIKRNVRKSSGRGELLISLCYQSTTNTL 304
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GENERAL INFORMATION:
APPLICANT: French, Cynthia K.
APPLICANT: French, Cynthia K.
APPLICANT: Stoneider, Patrick A.
APPLICANT: Yamamoto, Karen K.
TITLE OF INVENTION: Prostate Cancer-Specific Marker
NUMBER OF SEQUENCES: 27
CORRESPONDENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 94111-3834

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/036,315
FILING DATE: 06-MAR-1998

CLASSIFICATION NUMBER: US 60/047,811
FILING DATE: 15-MAY-1997

PRIOR APPLICATION NUMBER: US 60/047,811
FILING DATE: 07-MAR-1997

RIGHT APPLICATION NUMBER: US 60/041,246
FILING DATE: 07-MAR-1997

ATTORNEY/AGENT INPORMATION:
NAME: SCOCTIAL JOHN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 226; DB 3; I
Pred. No. 4.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REPERENCE, DOCKET NUMBER: 018002-000210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 10.3%; Score 226; DE Local Similarity 100.0%; Pred. No. 4.8 nes 46; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
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RESULT 13

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154 LGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILP--EKKHKVKTRVL 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: Molz, Lisa
APPLICANT: Chen, Yen-Wen
TITLE OF INVENTION: No. 6291220el PI 3-Kinase Poly,
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/170,996
                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
FILING DATE: 29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.3%; Score 182.5; DB 2; Best Local Similarity 32.8%; Pred. No. 8.2e-11; Matches 39; Conservative 29; Mismatches 48;
                                                                                                                                                                                                                                                                                                       FILING DATE: 29-FEB-1996
CLASSIFICATION: 435
ATTORNEY AGEN B.
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 23,07K-063700US
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 2307K-063700US TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 29-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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This polypeptide is encoded by a newly isolated hormone-regulated gene, termed Repro-PC-1.0 (see AAVG7327), isolated from prostate cancer cells. The polypeptide (calculated mol.wt.48,070, pI 8.83) contains 2 copies of a 116-amino acid repeat that show homology to the C2 regulatory domain of calcium-dependent isoforms of protein kinase c, and to isoforms of synaptotagmin. Repro-PC1.0 expression is specifically and differentially up-regulated in INCaP tumour cells. The invention provides methods of identifying hormone-regulated traits in a cell. The methods involve cultivating the cell as a graft in 2 different hormonal environments and determining whether expression of the trait differs in the 2 grafts. The methods can be used to identify chormonally-regulated traits and hormonally-regulated genes for use as targets for therapeutic intervention in disease states,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 PAMDEQSWISDPYIKOTILPEKKHKVKIRVLRKTLDPAFDEIFFFGIPYTQIQELALHF
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мерго-Рс-1.0; prostate cancer; LNCaP; hormone-regulated
human; synaptotagmin.
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                                                                                                                                           Repro-PC-1.0 is a novel prostate cancer-specific marker, which represents a novel human brain synaptoragmin isoform that may function in excytosis and endocytosis pathways. Its amino acid sequence was deduced from CDNA clones (see AAV54208) isolated from cancer from CDNA clones (see AAV54208) isolated from CDNA clones (see AAV54208) isolated from CDNA clones (see AAV54208) isolated from CDNA clones (see AAV54208) isolated from CDNA clones (see AAV54208) isolated from CDNA clones (see AAV54208) isolated from CDNA clones or a Class II MMC-restricted cytotoxic T-lymphocyte response or a Class II MMC-restricted control of CDNA control of CONTROL of CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL
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              for the detection and prophylactic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone-regulated Repro-PC-1.0 polypeptide.
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                                                                                              Claim 1; Page 68-69; 87pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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354 TLNPIFNESFIYDIPTDLLPDISIEFLVIDFDRTTKNEVVGRLILGAHSVTASGAEHWRE 413
                       1 MAEITNIRPSFDVSPVVAGLIGASVLVVCVSVTVFVWSCCHQQAEKKHKNPPYKFIEMIK
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                                                                                GVDIYPENLNSKKKF-----GADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPG
                                                                                                                        ----KDPRGPS
                                                                                                                                                                                                                                                                       174 LVYTIQEAHGLPVMDDQTQSSDPYIKWTILPDKRHRVKTRVLRKTLDPVFDETFTFYGIP
                                                                                                                                                                                                                                                                                                                                                   294 BLQVSLSYQPVAQRMTVVVUKARHLPKMDITGLSGNPYVVVVYGRKRIAKKKTHVKKC
                                                                                                                                                                                                                                               170 FVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIP
                                                                                                                                                                                                                                                                                                                                230 YTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRG
                                                                                                                                                                                                                                                                                                                                                                                                              ELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLS-DPYVKVNLYHAKKRISKXKTHVKKC
MAPITISREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCORKSSKSNKTPPYKFVHVLK
                                                                                                                                                                 ---FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 TPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGA-AAEGTGGEHWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F, W
Zhang J;
                                                                                                                      61 GISİYPETLSNKKKIIKVRRDKDGPGREGGRRNLLVDAAEAGLLSRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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414 VCESPRKPVAKWHSLSE 430
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20000S-0620312.
20000S-0659450.
20000S-0662191.
20000S-062191.
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2000US-0552317.
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                                                                                                                                                                   SPSDLENATPKL-
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19-JUL-2000;
03-AUG-2000;
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25-APR-2000;
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Wang J, 1
Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.
                                                                                                          420
                                                                                                                                                                                        DIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICDYPRRQIAKWH 420
                       TILSFDRFSRDDIIGEVLIPLSGIELSEGKMI,MNREIIKRNVRKSSGRGELLISLCYQST 300
TILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQST
                                                                                  TNTLTVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKR1SKKKTHVKKCTPNAVFNELFVF
                                                                                                                                                                   DIPCEGLEDISVEFLVLDSERGSRNEVIGOLVLGAAAEGTGGEHWKEICDYPRROIAKWH
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primers useful for synthesizing full length cDNA clones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%; Score 1162; DB 22; 52.4%; Pred. No. 2.8e-99; iive 77; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide, SEQ ID NO: 3040.
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08-JUL-1999; 99JP-0194486. 11-JAN-2000; 2000JP-0118774. 02-MAY-2000; 2000JP-0183765.

(HELI-) HELIX RES INST

07-JUL-2000; 2000EP-0114089

Homo sapiens

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in genetic manipulation

2001-524255/58

N-PSDB; AAK94341

Conservative

Best Local Similarity Matches 229; Conserv

Query Match

431 AA;

Seguence

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the encoded polypeptides (AAM38642-AAM42213) with nootropic, mamunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TINPIENESFIYDIPTDELEDISIEFLVIDEDRTTKNEVVGRLILGAHSVTASGAEHWRE 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVDIYPENLNSKKKF-----GADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLLISLCYQSTINTLTVVVLKARHLPKSDVSGLS-DPYVKVNLYHAKKRISKKKTHVKKC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPNAVFNELFVFDIPCEGLEDISVEFLYLDSERGSRNEVIGQLVLGA-AAEGTGGEHWKE 407
                                                                                                                                                                                                                                                         system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVVIIQEAHGLEVMDDQTQGSDPYIKMTILPDKRHRVKTRVLRKTLDPVFDETFTFYGIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAEITNIRPSFDVSPVVAGLIGASVLVVCVSVTVFVWSCCHQQAEKKHKNPPYKFIHMLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GISIYPETLSNKKKIIKVRRDKDGPGREGGRRNLLVDAAEAGLLSRD-----KDPRGPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKA
                                                                                                                                                            invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.8%; Score 1162; DB 22; Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.4%; Pred. No. ...
rive 77; Mismatches 111;
                                                                                                                   Example 4; SEQ ID NO 2722; 10078pp; English
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WPI; 2001-442253/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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The present invention relates to human secretion and trafficking (SAT)

proteins and their corresponding polynucleotides. SAT DNAs and proteins
are useful for diagnosing, treating and preventing vesicle trafficking
disorder (e.g. cystic fibrosis, diabetes mellitus, Grave's disease),
gastrointestinal disorders (e.g. hypertension, polymyositis), neurological
associated with transport (e.g. hypertension, polymyositis), neurological
disorders associated with transport (e.g., Alzheimer's disease, dementia,
depression, epilepsy, Tourette's disorder), cell proliferative disorders
(e.g. cirrhosis, cancer), autoimmune or inflammatory disorders (e.g. AlDS
(e.g. cirrhosis, cancer), autoimmune or inflammatory disorders (e.g. AlDS
(e.g. cirrhosis) and other disorders associated with transport such as
atherosclerosis) and other disorders associated with transport such as
sickle cell anaemia and hyperglycaemia. SAT proteins are useful in a
number of drug screening techniques and to analyse the proteome of a
cirsue or cell type. SAT DNAs are useful for creating knockin humanised
animals or transgenic animals to model human diseases, in somatic or
germline gene therapy, to generate a transcript image of a tissue or
cell type, for detecting differences in the chromosomal location due
to translocation, inversion, etc., among normal, carrier or affected
cindividuals, and as hybridisation probes for mapping naturally occurring
genomic sequences. The present sequence is human SAT-9 protein.
                           Human; secretion and trafficking protein-9; vesicle trafficking disorder; SAT-9; cystic fibrosis; diabetes mellitus; gastrointestinal disorder; Grave's disease; ulcerative colitis; cardiac disorder; hypertension; polymyositis; neurological disorder; Alzheimer's disease; dementia; depression; epilepsy; Tourette's disorder; cell proliferative disorder; cirrhosis; cancer; autoimmune disorder; inflammatory disorder; ALDS; acquired immune deficiency syndrome; Addison's disease; allergy; asthma; atherosclerosis; sickle cell anaemia; hyperglycaemia; transgenic animal; gene therapy; hypotensive; noctropic; neuroprotective; antidepressant; anticonvulsant; neuroleptic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secretion and trafficking polypeptide, useful in diagnosis, prevention and treatment of vesicle trafficking, transport, neurological, autoimmune/inflammatory, and cell proliferative disorders
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Bandman O, Elliott VS, Nguyen DB, Burrill JD, Marcus GA;
Zingler KA, Yao MG, Gururajan R, Ding L, Warren BA, Thangavelu K;
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|Tabel= Transmembrane_domain
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/label= C2_domain
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/label= C2_domain
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10-OCT-2000; 2000US-239384P.
28-NOV-2000; 2000US-253639P.
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SON COURSE OF COURSE NO COURSE NO COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF COURSE OF CO
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Seguence

Human secretion and trafficking protein-9 (SAT-9).

(first entry)

22-APR-2002 AAE17500;

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                                                                                                 GVDIYPENLNSKKKF----GADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPG
                                                                                                                  GISIYPETLSNKKKIIKVRRDKDGPGREGGRRNLLVDAAEAGLLSRD-----KDPRGPS
                                                                                                                                                              SGSCIDQLPIXMDYGEELRSPITSLIPGESK-TISPSSPEEDVMLGSLIFSVDYNFPKKA
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                                                1 MAPITTSREEFDEIPTVVGIFSAFGLVFTVS--LFAWICCORKSSKSNKTPPYKFVHVLK
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                           Gaps
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                        20;
 Length 431;
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                        Indels
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Otsuki
tch 52.8%; Score 1162; DB 23; al Similarity 52.4%; Pred. No. 2.8e-99; 229; Conservative 77; Mismatches 111;
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A, Nagai B
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T, Wakamatsu
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11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
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09-JUN-2000; 2000JP-0241899
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                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide which comprises a 3'-end sequence, where the combination of the S'-end sequence, where the combination of the S'-end sequence; selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the cettion and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 represent human amino acid sequences; AAB92446 to AAH3632 represent oligonucleotides, all of which are used in the exemplification
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                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
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52.4%; Pred. No. 5.2e-99;
iive 77; Mismatches 111;
Claim 8; SEQ ID 11567; 2537pp + CD ROM; English
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Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention.
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22-OCT-2001

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the

WPI; 2001-318749/34

SEQ ID NO 6294

Human polypeptide

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7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cyrostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAEITHNIRPSFDVSPVVAGLIGASVLVVCVSVTVFVWSCCHQQAEKKHKNPPYKFIHMLK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVDIYPENLNSKKKF-----GADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKPG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPSDLENATPKL----FLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, auch as tateral scierosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemoteactic/chemokinetic activity, demonstratic/chemokinetic activity, damenostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostetic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 52.4%; Score 1154; DB 22; Length 486; Best Local Similarity 52.2%; Pred. No. 1.8e-98; Matches 228; Conservative 77; Mismatches 112; Indels 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ma Y, (Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 6294; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen R,
                                                                     nootropic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAI60519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.N.S disorders.
                                                                                                                                                                                                                                                                                    WO200153312-A1
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09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                        leukaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang J,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                     Homo
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407
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                                             170 FVVNIKEARGLPAMDEQSMTSDPYIKWTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention siscloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                      TLNPIFNESFIYDIPTDILIPDISIEFLVIDFDRTTKNEVVGRLILGAHSVTASGAEHWRE
                                                                230 YTOIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRG
                                                                                                                                                               ELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLS-DPYVKVNLYHAKKRISKKTHVKKC
                                                                                                                                                                                                                         TPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGA-AAEGTGGEHWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4329; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 4329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW
                                                                                                                                                                                                                                                                                                                                                                                       ABB59179 standard; Protein; 474 AA.
                                                                                                                                                                                                                                                                                                  : | : | | : : | | | | : 469 VCESPRKPVAKWHSLSE 485
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                                                                                                                                                                                                                                                                                  408 ICDYPRRQIAKWHVLCD 424
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions
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2000US-245316P

2001US-272923P 2001US-276565P

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27-0CT-2000; 2000US-243681P.
27-0CT-2000; 2000US-243683P.
31-0CT-2000; 2000US-24443P.
01-NOV-2000; 2000US-244995P.
02-NOV-2000; 2000US-24595P.
02-NOV-2000; 2000US-24533P.
                                                                                                        19-JAN-2001; 2001US-262994P.
                                                                                                                   LS-FEB-2001; 2001US-269056P.
                                                                                                                                                     07-SEP-2001; 2001US-318119P
                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                            02-NOV-2000;
                                                                                                                                         L5-MAR-2001;
  14;
                                                                                                                                                                                                                                                                                  304
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                                                                                                                                                                                                                                                           264
                                                                                                                                                                N----FPKTNLKPGSPSDLENATPKLFLEGEKE-SVSPESLKSSTSLTSEEKQEKLGTLF 158
                                                                                                                                                                               E---LSEGKWLMNREIIKRNVR-KSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVS 320
                                                                                                                                                                                                                                                                                                                       | :|: :::|| |::::| |:: :::|| |:: 305 EIGDISKEALIVVILKARNLPRMDVT 364
                                                                                                                                                                                                                                                                                                                                                       GLSDPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIP-CEG----LEDISVEFL 375
                                                                                                                                                                                                                                                                                                                                                                            365 GLADPÝVKIYLLIYNGQRIAKKKTHVKKRTLSPVFNESFAFDIPAAEGAGASLEGVSLELM 424
                                                                                                                   -----SLHLDLEKRDLNG 103
                                                                     54
                                                                                            71
                                                                                                                                  (85 FKLRYLAERNALMVSIIRCRGLPCKGGSSGTGDIPTGMYGRTQAATDPYVKLQLLPDKQH
                                                                                                                                                                                                                                                                                245 KVKTRVVRNTRNPVYDEDFTFYGLNMNDLONMSLHFVILSFDRYSRDDVIGEVVCPLTSI
                                                                                           VPAILGLTAA----AVLSSVACICARQMRLRNKKQSQHDASFPFQPTRRPTAVRSPSGQP
                                                                                                                                                                                                              159 FSLEYNFERKAFVVNIKEARGLPAMDEQSMT------SDPYIKMTILPEKKH
                                                                                                                                                                                                                                                           KVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGI
                                              Gaps
                                              70;
                                                                                                                                                                                                                                                                                                                                                                                                    422
                          Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                   VLDSERGSRNEVIGOLVLGAA-AEGTGGEHWKEICDYPRROIAKWHVL
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                     14 IPTVVGIFSAFGLVFTVSLFAMICCQ-----RKSSKSNKTPPYKFV-
                       34.4%; Score 757; DB 22; 38.2%; Pred. No. 1.6e-61; tive 82; Mismatches 137;
                                                                                                                   -HVLKGVDI YPENLNSKKKFGADDKNEVKNKPAVPKN---
                   Ouery Match
Best Local Similarity 38.2°
Matches 179; Conservative
474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    376
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  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 fully defined sequences of 43-990 amino acids given in the specification. The NOVX polypeptide, nucleic acid and antibody of the invention are useful for treating or preventing a pathological condition in humans with a NOVX-associated disorder, e.g. Von Hippel-lindau syndrome, cirrhosis, transplantation disorders, pancreatitis, obesity, diabetes, autoimmune disease, renal artery stenosis, interstitial nephritis, glomerulonephritis, polycystic kidney disease, cataract, Alzheimer's disease, acoustic trauma, cancer, infertility,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new polypeptide that comprises any of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiomyopathies, atherosclerosis, hypertension, congenital heart defects, soleroderma, eatherosclerosis, hypertension, congenital heart defects, soleroderma, endometriosis, hypertension, congenital heart barkinson's disease, endometriosis, namentia, stroke, solerosis, anxiety, pain, leukaemias, hypothyroidism, psoriasis, acne, wounds and aethma. They are also useful for the manufacture of a medicament for treating a syndrome associated with a human disease, specifically a NOWX-associated disorder. They may also be useful in therapeutic applications including protein therapy, as small molecule drug targets, as antibody targets, as diagnostic and/or prognostic markers, in gene therapy, as research tools and in tissue regeneration. The present amino acid sequence represents one of the 17 novel proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 VPTVSL-----FAMIC--CORKSSKSNKTPPYKFVHVLKGVDIYPENLNSKKKFGADD--
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Casman S, Blalock A, Li L;
rtak K, Gerlach V, Edinger S;
ithson G, Gunther E, Padigaru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71; Gaps
                                                                                                                                                                                                                                                                                       Isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing, diagnosing and researching pathological conditions in humans with a NOVX-associated disorders, e.g. cancer, estroke or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.3%; Score 622.5; DB 23; Length 403; 36.2%; Pred. No. 4.1e-49;
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   Spytek KA, Gilbert J, Casman S, Shenoy S, Mishra V, Furtak K, G Stone D, Millet I, Smithson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 IITVSLSVTVVLCGLCHWCORKLGKRYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 46; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 153; Conservative
                                                                      U, Stone .,
I, Anderson D;
                                                                                                                                                                                      2002-590673/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                            N-PSDB; ABK51682
                                     Vernet CAM,
Malyankar U,
Taupier RJ,
Gangolli EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
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Von Hippel-Lindau syndrome; cirrhosis; transplantation disorder; von Hippel-Lindau syndrome; cirrhosis; transplantation disorder; pancreatitis; obesity; diabetes; autoimmune disease; infertility; renal artery stenosis; interstitial nephritis; glomerulonephritis; polycystic kidney disease; carract; Alzheimer's disease; cancer; acoustic trauma; cardiomyopathy; atherosclerosis; hypertension; compenital heart defect; scleroderma; endometriosis; haemophilia; dementia; stroke; Parkinson's disease; Huntington's disease; epilepsy; multiple sclerosis; anxiety; pain; leukaemia; hypothyroidism; psoriasis; acne; wound; asthma; human disease; calpain; epsin; zinc finger; low density lipoprotein B; IDLB; purinoceptor; CG8841; synaptotagmin; serine protease TLSP; mitogen activated protein kinase kinase-2; glypican-2 precursor; thymosin beta-10.

26-OCT-2001; 2001WO-US50925 26-OCT-2000; 2000US-243320P. 26-OCT-2000; 2000US-243592P.

WO200255702-A2

Homo

18-JUL-2002

Human; NOVX; pathological condition; NOVX-associated disorder;

Human Synaptotagmin-like protein #2.

(first entry)

05-NOV-2002

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ABG70275;

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ABG70275 standard; Protein; 403

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180 LPAMDEOSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQELALH 239

9;

Gaps

144 112 211 232

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113 GSPSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAPVV 172
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                                                                                                                                                                                                                                                                                                                                                                                                                  ----DKQSEQKLGRINFKLEYDFNSNSLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AMNKTLVFALFDFDRFSKHDQIGEVKVPLCTIDLAQ-TIEEWRDLV--SVEGEGGGEKLG
                                                                                                                                                                                                                53 FYHYLKGYDIYPENLINSKKKFGADDKNEVKNKPAVPKNSLHLDLEKRDLNGNFPKTNLKP
                                                                                                                                                                                                                                                                                    ---VDMKSVQLLGSAYKEKVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 NIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 DICFSLRYVPTAGKLTVVILEAKNLKKMDVGGLSDPYVKIAIMQNGKRLKKKKKTSIKKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 PNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEIC
                                                                      ---GIFSAFGLVFTVSLFAWICCORKSSKSNKTPPYK
                                                                                                                                          PVIKKIEHVGEVVTEVIAERTGLPTWGVVAIIILVFLVVFGIIFFCVRRFLKKRRTK---
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73;
   144;
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   Mismatches
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   67;
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2000US-0184664
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151;
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                                                                                                                                                                                                                                                                                                                                                                                                       FDIPCEGLEDISVEFLVLDSERGSRNEVIGGLVLGAAAEGTGGEHWKEICDYPRRQIAKW 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
   LQVLDYDRFSRNDPIGEVSIPLNKVDLTQ--MQTFWKDLKPCSDGSGSRGELLLSLCYNP
                                                                                                                                                                                                                                                                                                      SANSIIVNIIKARNIKAMDIGGISDPYVKVWLMYKDKRVEKKKTVTMKRNINPIFNESFA
                                                                                                               240 FTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQS
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Pred. No. 5.3e-49;
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Adams M,

JC,

Venter

(PEKE ) PE CORP NY

WPI; 2001-656860/75

N-PSDB; ABL03763

interactions

23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150. 23-MAR-2001; 2001WO-US09231

28.3%;

Query Match Best Local Similarity

474 AA

Sequence

(ABB57737-ABB72072).

349

ABB59660 standard; Protein; 474 AA.

RESULT 10 ABB59660

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(first entry)

26-MAR-2002

Drosophila melanogaster.

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27-SEP-2001

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08-SEP-2000; 20000S-0222081.
12-SEP-2000; 20000S-0231968.
14-SEP-2000; 20000S-0232397.
14-SEP-2000; 20000S-0232399.
14-SEP-2000; 20000S-0232400.
14-SEP-2000; 20000S-0232401.
14-SEP-2000; 20000S-0233063.
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30-AUG-2000; 2000US-022824.
01-SEP-2000; 2000US-0229343.
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08-SEP-2000; 2000US-0232080.
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06-SEP-2000; 2000US-0230433.
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29-SEP-2000;
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Ruben SM;
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2000US-0249264.
2000US-0249265.
2000US-0249297.
2000US-0249300.
2000US-025100.
2000US-0251030.
2000US-0251030.
2000US-0251030.
2000US-0251030.
2000US-0251030.
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2000US-0246611.
2000US-0249207.
2000US-0249208.
2000US-0249209.
2000US-0249210.
2000US-0249210.
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2000US-0249213.
2000US-0249214.
2000US-0249214.
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2000US-0249217.
2000US-0249218.
2000US-0249248.
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                                                                        2000US-0241826.
2000US-0246474.
2000US-0246474.
2000US-0246476.
2000US-0246477.
2000US-0246477.
2000US-0246523.
2000US-0246523.
2000US-0246525.
2000US-0246525.
2000US-0246525.
2000US-0246525.
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2000US-0246609.
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20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OC
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08-NOV-2000; 2
10-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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17-NOV-2000; 2
17-NOV-2000; 2
17-NOV-2000; 2
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17-NOV-2000; 2
17-NOV-2000; 2
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17-NOV-2000;
17-NOV-2000;
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used as New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and food additives or preservatives -

Claim 9; SEQ ID No 772; 837pp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polyheptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative

Drmanac RT;

Wang D,

Wang J,

Wehrman T,

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8
disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral isobaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amgiogenesis, nervous system disorders e.g. Alzheimer's disease and amgiogenesis, nervous system disorders e.g. dysphagia, e.g. organifection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrom, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pitulitary dwarfism, cancers and disorders e.g. malignancies, leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders end blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 QEMITVVVILKARHLPKMDITGLSGNPYVKVNVYYGRKRIAKKKTHVKKCTLNPIFNESFIY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 NTLTVVVLKARHLPKSDVSGLS-DPYVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVF 360
                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVRKSSGRGELLISLCYQSTT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VLSFDRFSRDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRNIQKCISRGELQVSLSYQPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGA-AAEGTGGEHWKEICDYPRRQIAKW
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                 Length 195;
                                                                                                                                                                                                                                                                                                                                                                                                    32; Indels
                                                                                                                                                                                                                                                                                                                                                              Query Match 27.9%; Score 614; DB 22;
Best Local Similarity 59.5%; Pred. No. 8.7e-49;
Matches 110; Conservative 41; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 HVLCD 424
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RESULT 12

antiarthritic.

Homo sapiens.

W0200270539-A2.

12-SEP-2002.

05-MAR-2001; 2002WO-US05095.

05-MAR-2001; 2001US-0799451.

(HYSE-) HYSEQ INC.

Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Z Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z,

Ren F;

Zhao QA,

Ghosh M;

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ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP6892-ABP68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lugus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, parasitic), arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antilipaemic; neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 LKAFDLPAKDFCG-SSDFYVKIYLLPDRKCKLQTRVHRKTLNPTFDENFHF-PVPYEELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 PSDLENATPKLFLEGEKESVSPESLKSSTSLTSEEKQEKLGTLFFSLEYNFERKAFVVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 KEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKTLDPAFDETFTFYGIPYTQIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 ELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMNREIIKRNVR----KSSGRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 ILISLCYOSTINTLIVVVLKARHLPKSDVSGLSDPYVKVNLYHAKKRISKKKTHVKKCTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 NAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLGAAAEGTGGEHWKEICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide (I) comprising a
New polynucleotides comprising sequences assembled from expressed sequence tags (ESTB), useful for treating cell-proliferative, neurodegenerative, autoimmune, generic, myeloid or lymphoid, or platelet or coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 418;
                                                                                                                                           Claim 9; SEQ ID NO 1367; 1012pp + Sequence Listing; English
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27.7%; Score 609; DB 23; Length 4:
Best Local Similarity 41.0%; Pred. No. 7.9e-48;
Matches 129; Conservative 62; Mismatches 104; Indels
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ABJ04645
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16;

Gaps

72;

Indels

159; Conservative

Similarity

Query Match Best Local S: Matches 159

20 IFSAFGL-VFTVSLFA-WICCQRKSSKSNKTPPYKFVHVLKGVDIYPENLNS--KKKFGA

-----WPCWKSKPVTSNITTLPQSISSAPTEVFET

76 DDKNEVK--NKPAVPKNSLHLDLEKRDLNGNFP---KTNLK----

60 VVŠFCGLALLVVŠLFVFWKLĊ-

셤

ð 9 ð 269

210 VLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEG

287 VHRKTLNPLFDETPQF-PVAYDQLSNRKLHFSVYDFDRFSRHDMIGEVILD----NLFEV

염

270 KMLMNREIIKRNVR----KSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDP 342 SDLSREATVWKDIHCATTESIDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDP YVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRN 

326 402 386

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В ₽

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286

209

153 227

--DLENATPKLFLEGEKES----VSPESLKSSTSLTSEEKQEK

S--S

116

셤

154

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g ð

169 TRHSSFRRHLPRQMQVSSVDFSMGTEPVLQRGETTTSIGRIKPELYKOK-SVDSEGNONE ----LGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTR 228 DVKICGKINFTLOYDYENELLVVKIIKALDLPAKDFTG-TSDPYVKMYLLPDRKKKFOTR 385

461

EVIGOLVLGAAAEGTGGEHWKEICDYPRRQIAKWHVLCD 424

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AA019183 standard; protein; 533

RESULT 14 AA019183

325

401

341

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対策級発音性性対象などとととととととととととととととだけだ
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anti-HIV; antiallergic; antirheumatic; antiarthritic; NOVX; diabetes; metabolic disorder; obesity; infectious disease, Alzheimer's disease; ancerais, neurodegenerative disorder; Parkinson's disorder; obesity; immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease; metabolic syndrome X; wasting disorder; cancer; neurological disorder; epilepsy; stroke; mental disorder; schizophrenic disorders; goiter; vesicular transport; cystic fibrosis; gastrointestinal disorder; multiple sclerosis; theumatoid arthritis; transgenic animal; ranquiliser; neuroleptic; antidiabetic; antiulcer; antiinflammatory; gene therapy

Unidentified

WO200246409-A2

13-JUN-2002

06-DEC-2001; 2001WO-US46586

06-DEC-2000, 2000US-251660P. 12-DEC-2000, 2000US-255029P. 08-JAN-2001; 2001US-26326P. 24-JAN-2001; 2001US-263800P. 20-FEB-2001; 2001US-269942P. 24-APR-2001; 2001US-286183P. 20-AUG-2001; 2001US-286183P.

2001US-318712P 12-SEP-2001;

(CURA-) CURAGEN CORP

Guo X, Li L, Patturajan M, Shimkets RA, Casman SJ, Malyankar UM Tchernev TY, Vernet CAM, Spytek KA, Shenoy SG, Alsobrook JP; Sdingers S, Peyman JA, Stone DJ, Ellerman K, Ganglli EA; Boldog FL, Colman SD, Elsen AJ, Liu X, Padigaru M, Spaderna SK; Casman SJ, Malyankar UM; Zerhusen BD;

WPI; 2002-547774/58. N-PSDB; ABT05458.

ö Novel isolated polypeptide, designated NOVX, useful for treating opreventing cancer, diabetes, obesity, dyslipidemia, anorexia, and metabolic, neurodegenerative, immune and hematopoietic disorders

Claim 1; Page 53; 421pp; English

Human; neurotransmission-associated protein; NTRAN; autoimmune disorder; inflammatory disorder; cancer; cardiovascular disorder; infection; neurological disorder; metabolic disorder; immunomodulatory; nootropic;

Human neurotransmission-associated protein NTRAN6.

(first entry)

27-NOV-2002

AA019183;

neuroprotective; antiinflammatory; cytostatic; cardiant; gene therapy

The invention relates to an isolated polypeptide, designated NOVX, comprising a sequence fully defined in the specification. The isolated protein, its encoding polynucleotide or an antibody created from the protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder in a subject, preferably human. The isolated protein its encoding polynucleotide or an antibody created from the protein are also useful to polynucleotide or an antibody created from the protein are also useful or treating or preventing metabolic disorder, hasematopoietic disorders, and various disease, neurodegenerative disorder. Alzheimer's disorders, and various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X, wasting disorders associated with chronic diseases, and cancer. The isolated protein, its encoding chronic diseases, and cancer. The isolated protein are useful for chronic diseases, and cancer. The isolated protein are useful for chronic diseases, and cancer. The isolated protein are useful for treating or preventing menciogical disorders such as epilepsy, stroke, mental disorders including mood, anxiety, schizophrenic disorders, dispetes mellitus, goiter, gastrointerinal disorders including ulcerative colitis, other conditions associated with abnormal vesicle trafficking including AIDS, allergic reactions, multiple sclerosis and rheumatoid arthritis. A cell comprising the vector of the invention is useful for producing non-human transgenic animals. The polymucleotide of the invention can be used to treat disorders by gene therapy. This sequence represents one of the isolated NOVX proteins of the invention.

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Bauqhn MR;
                                                                                                                           Ison CH, Thangavelu K, Lu DAM,
Warren BA, Lee EA, Griffin JA;
                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                           f, Honchell CD,
Yue H, Tang YT,
IJ, Walia NK;
                                                                                                                                               WPI; 2002-674945/72.
                                                                                                                                                    N-PSDB; AAL49656
                                                                                                                                      Forsythe IJ,
                                                                                                                            Duggan BM,
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Sequence

16-FEB-2001; 2001US-269748P. 11-MAY-2001; 2001US-290524P. 19-OCT-2001; 2001US-343742P.

15-FEB-2002; 2002WO-US04536.

WO200266646-A2.

29-AUG-2002

Homo sapiens

us-09-680-121c-2.rag

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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                               Tang YT,
               30-MAR-2001; 2001WO-US08631
                                              31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1295 AA;
                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                  N-PSDB; AAS70768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -DLENATPKLFLEGEKES----VSPESLKSSTSLTSEEKQEK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YVKVNLYHAKKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRN 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of human neurotransmission-associated proteins NTRAN1, NTRAN2, NTRAN3, NTRAN4, NTRAN5, NTRAN6, NTRAN7 and NTRAN8. These can be used in the treatment of diseases associated with aberrant expression of NTRAN, such as autoimmune/inflammatory, cardiovascular, neurological, developmental, cancer, transport, psychiatric, metabolic and endocrine disorders. The present sequence is an NTRAN protein of the invention.
                             such
                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 DVKICGKINFTLQYDYENELLVVKIIKALDLPAKDFTG-TSDPYVKMYLLPDRKKKFQTR
                                                                                                                                                                                                                                                                                                                                                                                              60 VVSFCGLALLVVSLFVFWKLC------WPCWKSKPVTSNITTLPQSISSAPTEVFET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLRKTLDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDLSREATVWKDIHCATTESIDLGEIMFSLCYLPTAGRMTLTVIKCRNLKAMDITGSSDP
                                                                                                                                                                                                                                                                                                                                                                20 IFSAFGL-VFTVSLFA-WICCORKSSKSNKTPPYKFVHVLKGVDIYPENLNS--KKKFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                    -----BGSb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRHSSFRRHLPROMOVSSVDFSMGTEPVLORGETTTSIGRIKPELYKOK-SVDSEGNONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LGTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMT1LPEKKHKVKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMLMNREIIKRNVR----KSSGRGELLISLCYQSTINTLTVVVLKARHLPKSDVSGLSDP
                                                                                                                                                                                                                                                                                                                                  Gaps
               or
        New isolated NTRAN polypeptide, useful for diagnosing, treating or preventing diseases associated with aberrant expression of NTRAN, as autoimmune/inflammatory, cardiovascular, cancer, endocrine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                  Length 533;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 DDKNEVK--NKPAVPKNSLHLDLEKRDLNGNFP---KTNLK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVIGOLVLGAAAEGTGGEHWKEICDYPRRQIAKWHVLCD 424
                                                                                                                                                                                                                                                                                             27.7%; Score 609; DB 23; 34.6%; Pred. No. 1.1e-47; ive 73; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 155-156; 172pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #6572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG06581 standard; Protein; 1295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.6
Matches 159; Conservative
                                                             metabolic disorders
                                                                                                                                                                                                                                                              533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002
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                                                                                                                                                                                                                                                               Sequence
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The invention relates to isolated polymucleotide (I) and polymeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PKR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, foremsizes, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Committee and polymer data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1146 WKDLKPCSDGSGSRGELLLSLCYNPSANSIIVNIIKARNLKAMDIGGTSDPYVKVWLMYK 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1029 GRIQFSVGYNFQESTLTVKIMKAQELPAKD-FSGTSDPFVKIYLLPDKKHKLETKVKRKN 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- DINGNPPKTNLKPGSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 LDPAFDETFTFYGIPYTQIQELALHFTILSFDRFSRDDIIGEVLIPLSGIELSEGKMLMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 REIIKRNVRKSSGRGELLISLCYQSTTNTLTVVVLKARHLPKSDVSGLSDPYVKVNLYHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 KKRISKKKTHVKKCTPNAVFNELFVFDIPCEGLEDISVEFLVLDSERGSRNEVIGQLVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 DLEN--ATPKLF------OEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTLFFSLEYNFERKAFVVNIKEARGLPAMDEQSMTSDPYIKMTILPEKKHKVKTRVLRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 607.5; DB 22;
Pred. No. 5.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ENLNSKKKFGADDKNEVKNKPAVPKNSLHLDLEKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published pct sequences
Claim 20; SEQ ID No 36940; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  395 AAAEGTGGEHWKEICDYPRRQIAKWHVL 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.19
Matches 144; Conservative
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